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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Mus musculus histamine H4 receptor mRNA, complete cds.
AFJSBB59
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Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Direct Submission
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Homo sapi Sequence Sequence

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Result No.

AX376577 AX301229

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Mus musculus chromosome UNK clone RP23-314021, complete sequence.
AC131672
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
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                                                                                                                                            796 AGGAAGCTAGCCAGGTCACCTGCTTTTTGCCCATTTTGCCTCCA
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                          TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC
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Submitted (11-FEB-2004) Genome Sequencing Center, 4444 Forest
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On Feb 11, 2004 this sequence version replaced gi:38194370
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Center code: WUGSC
Web site:http://genome.wustl.edu
Contact: submissions@wastson.wustl.edu
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McPherson, J.D. and Waterston, R.H.
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identification sequence tag: GTGGTTA'
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Pred. No. 1.6e-277;
0; Mismatches 0;
                                                                      /note="synonyms: H4, H4R,
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Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L., Umland, S.P. and Wang, P. Polynucleotide encoding a histamine receptor
Patent: US 6204017-A 1 20-MAR-2001;
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                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
/mol_type="unassigned DNA<sup>r</sup>
                                                                                   Sequence 1 from patent US 6204017.
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1. .1173
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                                                                                                                                                                                                                                                                 GIGTCTTATAGGGCTCAACACACACACACATGAAGATTGTTGCTCAAATGGTGGCTGTT
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                                                                                                                                                                                           Score 821.4; DB 6; Length
Pred. No. 3.4e-271;
0; Mismatches 36; Indels
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                                                     1. .1998D.
/ organism="Mus musculus"
/ organism="Mus musculus"
/ mol_type="genomic DNA"
db_xref="taxon:10090"
/ chromosome="UNK"
/ chone="RP23-314021"
project name: M_BA0314021
                                   Location/Qualifiers
                                                                                                                                                                                         Query Match
Best Local Similarity 95.9%;
Matches 843; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGATTCTTGGAAGAACAGC 480
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                                                                                                                                                                                                                        Length 1173;
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                                                                                                                                                                                                                        Score 686.6; DB 2;
Pred. No. 4.1e-225;
                                                                                                                                                                                                                                                                                   0; Mismatches 284;
                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Location/Qualifiers
                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.1%;
Matches 886; Conservative
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JP 2001211889-A/1
07-AUG-2001
27-GCT-2000 JP 2000328359
27-GCT-1999 GB 9925641:4,20-APR-2000 GB 0009973:9 PI PETER, MARK ANTONY OLAYLEE
C12N15/09, A61X38/00, A61X39/395, A61X39/
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                                       714
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGAATCTCTT
                                                                                                     961 TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG
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1 (bases 1 to 1173)
Peter, B. and Olaylee, M.A.
Novel polypeptide
Patent: JP 2001211889-A 1 07-AUG-2001,
PFIZER INC
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A61K37/02,C12N5/00
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Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L., Umland, S.P. and Wang, S.
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Pred. No. 4.1e-225;
0; Mismatches 284;
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Patent: US 6613533-A 1 02-SEP-2003;
Schering Corporation; Kenilworth, NJ
Location/Qualifiers
1, 1173
/organism="unknown"
/mol_type="genomic DNA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                 TCATICITIGGAATTCGIGATCCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT
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                                                          -- TGAAGGTAGTGAATGTGAACCTGGATTTTTTTTTGGAATGGTACATCCTTGCCATCACA
                                                                                   541 ATGCTCTTGGAATTCCTGCTTCCTGTCTCTCTGTGGCTTATTTCAATGTACAGATTTAC
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                                                                                                                                                                                                                                                                                                                                             AGGAAGCTAGCCAGGTCACTGGCCATCCTTTGAGCGCTTTTTGCCTGGGCTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                    Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L.,
GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGAAGGA
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Histanine receptor
Patent: WO 0125432-A 112-APR-2001;
SCHERING CORPORATION (US)
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                                                      Gaps
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6
       Length 1173;
  Score 686.6; DB 2; Length
Pred. No. 4.1e-225;
0; Mismatches 284; Indels
Query Match 58.4%;
Best Local Similarity 75.1%;
Matches 886; Conservative
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us-10-626-445.5.rge

Db 421 GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGA 476  Qy 481 ACGAACACAAAGGACTGTGAACCTGGCTTTGTTACAGTGTACATCTTACACATTACA 540  Db 477TGAAGGTACTGTGAACCTGGATTTTTTTTTGTACAATGGTACACTTACA 534	541	Qy 601 TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT 660	DD 655 GTCTTTCACACATCTGTGACATCATCAGGGGAAACTCTTTAGGGGGAAACTCTTTAGGGGGAAACTCTTTAGGGGGAAACTCTTTAGGGGGAAACTCTTTAGGGGGAAACTCTCAAAGAGATCTCTGAAACTCTCTAGAAACTCTCTAGAAACACTCTTTAGGGGAAACACACAC	
Db 955 TATTCTCTCTTCACAATTGTCCTTTCATTTTATTCTCTCAGCAACAGGTCCTAAATCAGTT 1014  Qy 1021 TGGTACAGATTGCCTTCTGGCTGCAATGGTTCAATTGTTAATCCCTTTCTGTAC 1080  nb 1015 HGGTACAGATTGCCTTCTGGCTAATTGTTTAATTCTTTTGTAATTCTTTTGTAATTCTTTTGTAATTCTTTTGTAATTCTTTTTGTAATTCTTTTTGTAATTCTTTTTTTAATTCTTAATTCTTTTTTTAATTCTTAATTCTTTTTT	1081 CCTTTGTGTCACAGGGTTTCCAGAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA	OY 1141 CCAGGGTGTCACAGAACCAGTCAGTATCTTTGA 1176		Db 301 TCTGTATATAACATTGTCCTCATCAGCTATGATCGATACTGTCAGTCTCTGAATGCTGTG 360  Qy 361 TCTTATAGGGCTCAACACTGGCATCATGAAGATTGTTGCTCAAATGCTGGCTG

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Hominidae; Homo.

1 (bases 1 to 1173)

Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A., Anthes, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonslorek, W., Shin, N., Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M. and Monsma, F.J. Jr.

Cloning and characterization of a novel human histamine receptor J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
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Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough
Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,
USA
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                    715 TCTGCATCGAGAAGTTCCTGCATCCTTTCATTCAGAGAGACAGAGGAGAAAGAGTAGT
                            661 ACCTCTTCCAGTGCTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT
                                                                                                                               GTCTCTTCCAACATCTGGGACACTCATTCAGGGCTAGACTATCTTCAAGGAGATCTCTT
                                                                                                                                                                           CCTGGATTGAAGGAATCAGCTGCATCTCGTCACAGAAAGTCCTCGAAGAAGAGCAGC
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        TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT
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Monsma,F.J. Jr., Wang,S., Behan,J., Laz,T.M., Greene,J. and
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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GSECEPGFESEWY ILAI TSFLEFVI PVILVAY FNNMI YWSLMKRDHLSRCQSHPGLTA
SKSI UTGHSFRGRLSSRRSLGASTEVDASFHSERQRRKSSLMFSRTKMNSNTTASKM
GSFGOSDSVALHQMFRUSLASTRLAKSLA ILLIGVFAVCWAPYSLFT VLSFYSSATG
PKSVWYRI AFWLQWFNSFVNPLLAYPLCHKRFQKAFLKI FCIKKQPLDSQHSRSVSST
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2 (bases 1 to 1173)
Zhu,Y., Michalovich,D. and Fitzgerald,L.R.
Direct Submission
Submitted (30-N0V-2000) GlaxoSmithKline, 709 Swedeland Rd., 1539, King of Prussia, PA 19406, USA
Location/Qualifiers
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                                                                                                                               1. .1173
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AXVUEZBU 1173 bp mRNA linear PRI 15-MAR-2004
Homo sapiens histamine receptor H4 (H4) mRNA, complete cds.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                                                                                                          895 AGGAGATTAGCCAAGTCACTGGCCATTCTCTTAGGGGTTTTTGCTGTTTTGCTGGGCTCCA
                                                                                                                                                                                            TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGCACCCCCAAATCGGTG
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                                                                                                                          AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA
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Nguyen, T., Shapiro, D. A., George, S.R., Setola, V., Lee, D.K., Chong, R., Rauser, L., Lee, S.P., Lynch, K.R., Roth, B.L. and O'Dowd, B.F.
Discovery of a novel member of the histamine receptor family Mol. Pharmacol. 59 (3), 427-433 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (26-SEP-2000) Pharmacology, University of Toronto,
Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada
Location/Qualifiers
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Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. O'Dowd, B.F.
Discovery of H4, a Novel Histamine Receptor
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                            1. .1173
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PKSVWYRIAFWLQWFNSFVNPLLYPLCHKRPQKAFLKTFCIKKQPLPSQHSRSVS"
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                                      'note="G-protein coupled receptor"
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larity 75.1%; Pred. No. 4.1e-225;
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GSECEPGFFSEWYILAITSFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTA
SKNICCHSPRRCRLSARTSCAFAFFWSFRKRKSLGAFSRFRYKNSTATASKM
GSFSOSDSVALHQMFFNELASATEVAKSLATILLGVPRVCMAPYSLFTIVLSFYSSATG
PKSVWYRIAFWLLARATLAKSLATILLGVPRVCMAPYSLFTIVLSFYSSATG
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Ads5125 Human H4
Ads5121 Human H4
Ads5121 Human H4
Ads6716 Human H4
Adu82889 Ligand up
Add5512 Human H4
Adu82889 Ligand up
Add5512 Human G-p
Aas98150 Human DNA
Ax84570 G-procein
Aaa70639 Rat G-pro
Aax84571 G-procein
Aaa70639 Rat G-pro
Aax84570 G-procein
Aaa70639 Rat G-pro
Aas84570 G-procein
Aaa70639 Rat G-pro
Aas84571 G-procein

## ALIGNMENTS

geneseqn1980s:\*

N\_Geneseq\_8:\* 1: geneseqn198 2: geneseqn199

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Database

The present sequence is that of a cDNA clone encoding a murine histamine receptor of the H4 subtype. The cDNA was isolated from a mouse spleen cDNA library. It shows 72.8% homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea claim 4; Fig 5A; 92pp; English. 8 X C C C C X Aai70981 Mouse his Add30257 Mouse GFC Aai70982 Rat hista Aa46023 Human GFD Aab8203 Human GFC Aah24007 Human GFC Ab78739 Nuclectid Ab78739 Nuclectid Aai70980 Human his Aca93262 Human cDN Ad988759 Human cDN Ad98759 Human end Ad988759 Human end Ad988750 Novel hum Ad98877 Novel human end Ad98837 Novel human end Ad98837 Novel human end Ad98837 Novel human end Ad98875 Human end Ad98875 Novel human end Ad98875 Novel human end Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AAI70981 AD30257 AAA4602 AAA4602 AAD01124 AAD78063 AAB78139 AAI70980 ACA93262 AAG98759 AAG98759 AAG98759 AAG98759 AAG98759 AAG98759 AAG987769 AAG987769 AAG987769 AAG987769 AAG987769 AAG987769 AAG987769 AAG98776 5: genesequ2002as:\*
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AAT AA170981; XX XX  18-MAR-2002 (first entry)  Examine H4 receptor cDNA.  Mouse histamine H4 receptor; mouse; antiasthmatic; antiallergenic; XX XX  Histamine H4 receptor; mouse; antiasthmatic; antiallergenic; XX XX XX  Mus musculus.  XX  06-DEC-2001.  XX  06-DEC-2001.  XX  06-DEC-2001.  XX  12-FEB-2001; 2001WO-US005914.  XX  XX  XX  XX  XX  XX  XX  XX  XX	i i	ID AAI70981 standard; cDNA; 1176 BP.
		AAI70981;
	X E X	Mouse histamine H4 receptor cDNA.
		Histamine H4 receptor: mouse: antiasthmatic: antiallergenic:
	_	antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
	<u>*</u>	diagnosis; gene therapy; ss.
		Mus musculus.
	X	
		WO200192485-Al.
		06-DEC-2001.
		22-FEB-2001; 2001WO-US005914.
		31-MAY-2000; 2000US-0208260P.
		(ORTH ) ORTHO-MCNEIL PHARM INC.
		WDI. 2002_114328/1E
		P-PSDB; AAMSOS6S.
		New mammalian histamine H4 receptor proteins and polynucleotides encoding
	_	the proteins, useful in gene therapy for treating diseases where it is
		beneficial to elevate mammalian histamine H4 receptor activity.
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Novel mammalian G protein coupled receptors, useful for identifying
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pig) histamine H4 receptor nucleic acid molecules (see AA170980-83) and polypoptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of histamine H4 receptor activity. Recombinant protein enammalian histamine H4 receptor activity. Recombinant protein H4 receptor. Such modulators of the mammalian histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D,
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condition
compounds that modulates diagnosing and treating disease conditior associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.
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Claim 151; SEQ ID NO 1360; 542pp; English

Sequences at least 94 identical to the GPCK proteins and nucleic acids associated with GPCRs of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR related diseases; a transgenic compounds useful in the treatment of GPCR related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgene or in an endogenous GPCR gene; cells derived from the transgene or in an endogenous GPCR gene; cells derived from the transgene or the invention; and kits comprising a mutation in a different GPCR gene of the GPCR polypeptides of which has comprising a mutation further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, darkhea, cells diseases or cohizophrenia); cellscasses including neurological disorders of the colon or intestine disorders of the adrenal gland; disorders of the colon or intestine conspection and signated disorders (e.g., autoimmune disorders (e.g., autoimmune disorders or ansemia or leuksemia); immune disorders; blood disorders or ALDS); bone and joint disorders (e.g., autoimmune disorders or ALDS); bone and joint disorders (e.g., autoimmune disorders or cohesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, cuterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and chrysish, skin, stomach, pancreas, spleen, thymus and cuterior or obtained in electronic format directly from WIPO at the principle of the invention of the principle of the invention of the principle of the invention of the present sequence represents a specent disorder of the present sequence represents a sequence of (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids invention relates to human and mouse G protein-coupled receptors ftp.wipo.int/pub/published\_pct\_sequences 

Seguence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0 Other;

ö 180 180 300 120 TTAATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAGCCTTT 120 240 240 420 421 TCTTATAGGGCTCAACACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGTTGTTTTGG 480 GACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCACGTGTTGTTTAACTGG 300 AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA 360 421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGATTCTTGGAAGAACAGC 480 9 GACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCACGTGTTGTTTAACTGG AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCCTTGGCATTT 61 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCCAGGTCCCCTTGGCATTT TCTTATAGGGCTCAACACACACGCATCATGAAGATTGTTGCTCAAATGGTGGTGGTTTGG Gaps ö DB 12; Length 1538; Indels . 0 Query Match
100.0%; Score 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 61 121 181 181 241 241 301 361 301 361 8 ઠે В ò 셤 δ ద ò 셤 ઠે 셤 ò 요

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	ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA		ATGCTCTTGGAATTCCTGCTGTCTCTCTGTGGCTTATTTCAATGTACAGATTTAC		TGGAGCCTGTGGAAGCGTCTCTCAGTAGTGCCCTAGCCATGCTGGATTCTCCACT		ACCTCTTCCAGTGCTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT		CCTGGATTGAAGGAATCAGCTGCATCTCGTCAGAAAGTCCTCGAAGAAGGAGCAGC		ATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGGTTCC		TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC		AGGAAGCTAGCCAGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGGCTCCA		TACTGTCTGTAAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG		TGGTACAGCATTGCCTTCTGGCTACGATGGTTCAATTCGTTTAATCCCTTTCTGTAC		CCTTTGTGTCACAGGCGTTTCCAGAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA		CCAGCGCTGTCACAGAACCAGTCAGTATCTTCTTGA 1176	
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AAI70982 standard; cDNA; 1176 BP 18-MAR-2002 (first entry) AAI 70982; RESULT 3 

Histamine H4 receptor; rat; antiasthmatic; antiallergenic; antiinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; ss.

Rat histamine H4 receptor cDNA

Rattus rattus

WO200192485-A1

06-DEC-2001.

22-FEB-2001; 2001WO-US005914.

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961 TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG 1020
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identification; agonist; screening; therapeutic; pharmaceutical; mutant;
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12-NOV-1998;
20-NOV-1998;
27-NOV-1998;
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                                                                                                                                                                                                                                                                                   New mammalian histamine H4 receptor proteins and polynucleotides the proteins, useful in gene therapy for treating diseases where beneficial to elevate mammalian histamine H4 receptor activity.
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Pred. No. 2e-289;
0; Mismatches 136; Indels 0;
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                                                                                  (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 5C; 92pp; English
                             31-MAY-2000; 2000US-0208260P
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Best Local Similarity 88.4%;
Matches 1040; Conservative
                                                                                                                                                                                                WPI; 2002-114339/15.
P-PSDB; AAM50566.
                                                                                                                                              Lovenberg T, Liu
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                              AATTITGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA
                                                                                                                                                                                                                                                                             421 Gigcicgcciictiagigaardagccaargarictagriicagagrciiggaagga----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535 TCATTCTTGGAATTCGTGATCCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT
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                                                                                                                                                                                                                                            TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       955 TATTCTCTGTTCACAATTGTCCTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes transmembrane receptors, preferably human grotein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen R,
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aw CW, Lin I, Lowitz K, White C;
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                      99US-0121852P
99US-0123944P
99US-0123946P
99US-0123948P
99US-0123948P
99US-0123948P
99US-0136436P
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12-MAR-1999;
12-MAR-1999;
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29-SEP-1999;
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28-MAY-1999;
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28-MAY-1999;
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03-SEP-1999;
29-SEP-1999;
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Score 686.6; DB 3; Pred. No. 4e-204; 0; Mismatches 284;

120 120 180 180 240 240 300

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420 420 480 476 534 600 594 999 654 720 714 780 774

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Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
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              transmembrane
                     Homo sapiens
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29-SEP-1999;
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12-OCT-1999
                                                                          16-FEB-1999
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TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG 1020
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Query Match 58.4%;
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Matches 886; Conservative
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G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned

C protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned

C pCR of the invention. Inke all GPCRs has seven transmembrane alpha

C helices with an extracellular N-terminus and an intracellular C-terminus.

However, no endogenous ligands has yet been identified for the proteins

C of the invention. The orphan GPCRs may be used in the identification of

their endogenous ligands, and to screen potential GPCR agonists and

antagonists for use as pharmaceutical agents. The proteins may also be

used in the study of GPCR-mediated signalling cascades, and to elucidate

their precise role in normal and diseased human conditions. Nucleic acid

encoding human orphan GPCRs may be used for tissue localisation

c expression analysis to provide information about their function in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists.
                                                              orphan G protein-coupled receptor; GPCR; hRUP7; drug screening;
embrane receptor; signal cascade; ss.
                                                                                                                                                                                                                                                               protein-coupled receptor"
                        orphan G protein-coupled receptor hRUP7 cDNA
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/product= "hRUP7"
/note= "Human orphan G
                                                                                                                                                                     Location/Qualifiers
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               TGGTATAGAATTGCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTTGTAT 1074
                                                      CCATTGTGTCACAAGGGCTTTCAAAAGGCTTTCTTGAAAATATTTTGTATAAAAAAGCAA 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     also useful for treating obesity, diabetes, metabolic, neurological diseases, psychotherapeutics, urogenital disease, reproduction and sexual medicine, inflammation, cancer, tissue repair, dermatology, photoageing, skin pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases, allergy and respixatory diseases, sensory organ disorders, sleep disorders and hair loss. The PFT-013 protein and nucleic acid are useful in the diagnosis and treatment of the above conditions and also for
                                                                                                                                                                                                                                                                                                  G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic; antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human; osteopathic; neuroprotective; nootropic; dermatological; gynecological; signal transduction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New G-protein coupled receptor-like polypeptide, polynucleotide for screening drug candidates for treating diseases associated with signal transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be expressed by standard recombinant methodology. Antibodies and modulators of PFI-013 are useful in the manufacture of a medicament for treating allergic disorder, including extrinsic asthma, immunological disorders, such as intrinsic asthma, vasculitic granulomatous disease, interstitial and other pulmonary disease, including chronic obstructive pulmonary disease (COPD), infectious, inflammatory disease, such as inflammatory bowel disease and neoplastic and myeloproliferative diseases. They are
                                      CCTTTGTGTCACAGGCGTTTCCAGAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA
CCTCTACCATCACAACACAGTCGGTCAGTATCTTTAA 1173
                                                                                             1141 CCAGCGCTGTCACAGAAC---CAGTCAGTATCTTCTTGA 1176
                                                                                                                                                                                                                                                                            Human GPCR-like polypeptide, PFI-013 encoding cDNA
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                                                                                                                                                                                           AAF83203 standard; cDNA; 1173
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20-APR-2000; 2000GB-00009973
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(PFIZ ) PFIZER INC.
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screening drug candidates for the treatment of diseases associated with signal transduction. The antibodies are also useful for enrichment of eosinophils from mammalian, especially human blood and for detecting the protein in biological samples
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                                                                                                                                                                                                                                           DB 4; Length 1173;
                                                                                                                                                                          Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
                                                                                                                                                                                                                                       Score 686.6; DB 4; Length Pred. No. 4e-204; O; Mismatches 284; Indels
                                                                                                                                                                                                                                           / Match 58.4%;
Local Similarity 75.1%;
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                                   961 TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG 1020
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                                                                                                                                                                                                                1075 CCATTGTGTCACAAGCGCTTTCAAAAGGCTTTCTTGAAAATTTTTGTATAAAAAAGCAA 1134
895 AGGAGATTAGCCAAGTCACTGGCCATTCTCTTAGGGGTTTTTTGCTGTTTGCTGGGCTCCA 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AXOR35; human; G protein-coupled receptor; 7TM receptor; histamine H3 receptor homologue; infection; viral; bacterial; fungal; protezon; H1V-2; pain; cancer; diabetee; obesity; anorexia; bulimia; osteoporosi; asthma; alergy; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcer; migraine; vomiting; psychotic disorder; neurological disorder; anxiety; schizophrenia; manic depression; bipolar disorder; depression; delirium; dementia; severe mental retardation; dyskinesia; Parkinson's disease; Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte; marcophage; eosinophil; neutrophil; function modulation; autoimmune disorder; pulmonary disorder; gene therapy; vaccine; drug screening; signal transduction; transgenic animal; drug discovery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma.
                                                                955 TATTCTCTGTTCACAATTGTCCTTTCATTTATTCCTCAGCAACAGGTCCTAAATCAGTT
                                                                                                         TGGTACAGCATTGCCTTCTGGCTGCATGGTTCAATTCGTTTGTTAATCCCTTTCTGTAC
                                                                                                                                          1015 TGGTATAGAATTGCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCTCTTTTGTAT
                                                                                                                                                                             CCTTTGTGTCACAGGCGTTTCCAGAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA
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                                                                                                                                                                                                                                                 1141 CCAGCGCTGTCACAGAAC---CAGTCAGTATCTTCTTGA 1176
                                                                                                                                                                                                                                                                     /product= "Human AXOR35"
/note= "G protein-coupled receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human G protein-coupled receptor AXOR35 cDNA.
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Michalovich D, Morrow DM, Zhu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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03-FEB-2000; 2000US-00497790.
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                                                                      The invention relates to the human G protein-coupled receptor AXOR35 (AAB73621), to cDNA encoding AXOR35 (AAB74006), and to AXOR35 fragments and variants. Like all G protein-coupled receptors, AXOR35 has reasonable and is involved in signal transduction. AXOR35 has homology and structural similarity with G protein-coupled receptors such as the human histamine H3 receptor. The invention also relates to expression vectors and host cells comprising AXOR35 DNA, to recombinant expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins and nucleotides may be used to treat a wide variety of disorders and nucleotides may be used to creat a wide variety of disorders including bacterial, fungal, protozoal and viral infections, particularly HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia; bullmia, osteoporosis; asthma, allergies; urinary retention; acute heart failure; hypotension; hypertension; angina
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                             Claim 2; Page 49-50; 54pp; English.
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/product= "Histamine receptor"

Location/Qualifiers

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This sequence represents the open reading frame for a human histamine receptor (HR) designated SP9144. The sequence was isolated by searching databases with the sequence of known G-coupled protein receptor (GCPR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoaffinity chromatography, in immunoassay of histamine receptor, to identify cDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis
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New nucleic acid encoding antigenic part of human histamine receptor, useful for preparing antibodies, e.g. for treating-histamine related

Example 1; Col 27-28; 19pp; English

disorders

Umland SP;

Monsma FJ, Morse KL,

Laz TM,

Behan JX, Hedrick JA, (SCHE ) SCHERING CORP

Wang S;

WPI; 2002-442063/47

P-PSDB; ABO98629

99US-00414010 99US-00414010

07-OCT-1999; 17-0CT-1999;

US6204017-B1

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Score 686.6; DB 6; Length 1173;
Pred. No. 4e-204;
0; Mismatches 284; Indels 9;
  ery Match 58.4%;
st Local Similarity 75.1%;
tches 886; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; histamine receptor; gene; ds; chromosome 18; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human histamine receptor coding sequence.
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psoriasis; receptor

Homo sapiens

300

420

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Gaps

6

Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

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961 TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG 1020
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                                     421 ATACTGGCTTTCTTGGTAAATGGCCCCGATGATTCTGGCTTCAGATTCTTGGAAGAACAGC
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Human; histamine receptor; receptor; inflammation; asthma; allergy; atopic dermatitis; stroke; myocardial infection; migraine; chronic obstructive pulmonary disease; COPD; rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease; psoriasis; inflammatory bowel disease; psoriasis; intracellular second messenger pathway; cellular growth rate;
                                                                                                                                      Nucleotide sequence of human histamine receptor.
                                 ABQ78739 standard; DNA; 1173
                                                                                                                                                                                                                                                                 hormone secretion; gene; ss
                                                                                                    05-DEC-2002
                                                                   ABQ78739
RESULT 9
                  ABQ78739
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9

180 240 300

241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300

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sapiens

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Novel mammalian histamine receptor polypeptide useful for identifying agonist or antagonist for treating diseases such as inflammation, asthma, stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human histamine receptor. The polypeptide is useful for identifying an agonist or antagonist of a mammalian histamine receptor. It is useful as an antigen to elicit the production of antibodies. The histamine receptor polypeptide and polymuclection useful in the treatment and management of diseases such as inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infection, migraine, chronic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis. They are also useful for modulating intracellular second messenger pathway activated through histamine receptors (cyclic-AMP, calcium, inositol phosphate and mitogen activated protein (MAP) kinase), changes in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TIAAIGICITCATITGCCTITGCTATAAIGGIAGGCAAIGCTGIGGICATCTTAGCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
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                                                            /product= "histamine receptor"
                                                                                                                                                                                                                                                                                                                                                         Monsma FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 15-16; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mobilization, mitogenic effects, etc
           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         Laz TM,
                                                                                                                                                           19-MAR-2001; 2001US-00812216.
                                                                                                                                                                                          99US-00414010
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Best Local Similarity 75.1%;
Matches 886; Conservative
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                                                                                                                                                                                                                        BEHAN J X.
HEDRICK J A.
LAZ T M.
MONSMA F J.
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-673827/72.
                                                                                                                                                                                                                                                                      MONSMA F J.
MORSE K L.
UMLAND S P.
                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ABB78276.
                                                                                                                                                                                                                                                       (LAZT/) LAZ T M.
(MONS/) MONSMA F
(MORS/) MORSE K
(UMLA/) UMLAND S
(WANG/) WANG S.
                                                                                             US2002098539-A1
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                                                                                                                           25-JUL-2002
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The present sequence is that of cDNA clone pH4R encoding a human histamine receptor of the H4 subtype. The cDNA was isolated from a bone marrow cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAT10980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Nammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the human histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, noninsulin dependent diabetes mellitus, hyperglycemia, constipation, arthythmia, disorders of the neuroendocrine system, stress and spasticity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.
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Pred. No. 4e-204;
0; Mismatches 284; Indels 9;
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75.1%;
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cardiant;
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Best Local Similarity
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DANG H T.
LIAW C W.
LIN I.
                                                                                                                                                                                                                                                                                                Chen R, Dang HT,
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26-FEB-1999
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The invention relates to a human G protein-coupled receptor (GPCR)
appearing as ABU92259-ABU92277 (encoded by CNMSA ACA93226-ACA93274) named
chare-1, hare-1, 
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standard; cDNA; 1173

ADG98759

RESULT 12

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The present invention provides novel human G protein-coupled receptor (GPCR) proteins and their encoding nucleic acids. The invention is useful tor making a probe for dor-blot analysis and for RT-PCR identification of the expression of the receptor in tissue samples. The invention is also useful for identifying candidate compounds as inverse agonists, agonists to partial agonists and as research tools in determining the location of the receptors within the body. The present sequence is human orphan G protein-coupled receptor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TTAATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAGCCTTT 120
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                                                            Human; G protein-coupled receptor; GPCR; research tool; gene;
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polynous and its included as an anti-AXOR35 antibody, an AXOR35 expression vector, producing a recombinant host cell by introducing the vector into a cell such that the host cell by introducing the vector into a cell such that the host cell by introducing the host cell expressing AXOR35, identifying/screening for agonists or antagonists of AXOR35 and inhibiting or promoting the function of lymphocytes, macrophages, cosinophils, or neutrophils in diseased tissue, by administering to the patient AXOR35 agonists or antagonist. The agonist or antagonist identified is useful for treating a disease such as asthma, or for inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue such as an asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays, for identifying compounds that are agonists or antagonists of AXOR35, as
                                                                                                                                                                                                                                                       Human; ss; gene; G-protein coupled receptor; AXOR35; lymphocyte; macrophage; eosinophil; neutrophil; infection; transplant rejection; gastrointestinal disorder; gastrio ulcer; inflammatory bowel disease; crohn's disease; irritable bowel syndrome; voniting; inflammation; atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis; psoriasis; urological disease; unimary retention; cardiovascular disease; myocardial infarction; hypotension; hypertension; pulmonary disorder; chronic obstructive pulmonary disease; cough; renal disease; nigraine; anoxesia; anxiety; schizophrenia; dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infections, gastrointestinal disorders, autoimmune disorders, urological diseases, cardiovascular diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated G-protein coupled receptor polypeptide, AXOR35, (and its homologues and variants) and its encoding polynucleotide (and its homologues, variants, complements and RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li X;
                                                                                                                                                                                                                     Human cDNA encoding G-protein coupled receptor AXOR35
1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCTTAA 1173
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vaccines, or for treating infections (bacterial, fungal, protozoan or viral infections), transplant rejection, gastrointestinal disorders (such viral infections), inflammatory bowel diseases (such as Crohn's disease), irritable bowel syndrome, vomiting, inflammation (such as atopic dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis, psoriasis), urological diseases (such as urinary retention), cardiovascular diseases (such as urinary retention), hypertension, pulmonary disorders (such as chronic obstructive pulmonary disease), cough, renal diseases (such as renal ischaemia); arteriosclerosis, atherosclerosis, psychotic and neurological disorders (such as migraine, anorexia, anxiety, schlzophrenia), dyskinesias (such as Parkinson's disease), cancer, obesity, stroke, septic shock, graft versus host disease and osteoporosis. The present sequence is the CDNA
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Pred. No. 4e-204;
0; Mismatches 284; Indels 9;
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Best Local Similarity 75.1%;
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                                                                                                       AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA
ATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Human endogenous orphan GPCR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human endogenous orphan G-protein coupled receptor RUP7 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-coupled receptor; GPCR; dot-blot analysis;
                                                                                                                                                                                                                                                                                                                   CCAGCGCTGTCACAGAAC --- CAGTCAGTATCTTCTTGA 1176
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .1173
                                                                                                                                                                                                                                                                                                                                                                                                             ВР
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99US - 0123949P.
99US - 0136437P.
99US - 0136439P.
99US - 0136567P.
99US - 01315567P.
99US - 013157P.
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99US-0120416P.
99US-0121852P.
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28-MAY-1999;
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CCATTGTGTCACAAGCGCTTTCAAAAGCCTTTCTTGAAAATATTTTTGTATAAAAAAGCAA 1134
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                                 541 ATGCTCTTGGAATTCCTGCTTCCTGTCATCTCTGTGGCTTATTCAATGTACAGATTAC
                                                 535 TCATICTIGGAATTCGTGATCCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTAT
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98US-0109213P.
98US-0110060P.
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12-NOV-1998;
20-NOV-1998;
27-NOV-1998;
16-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to human endogenous orphan G protein-coupled receptor (GPCR) proteins and polynucleotides encoding such proteins. The CDNA sequence of the human G protein-coupled receptor (GPCR) is useful in making a probe for dot-blot analysis against tissuemRNA and/or for RT-PCR identification of the expression of the receptor in tissue samples. GPCR sequences of the invention may be used in disease/disorder identification and/or selection, in screening of candidate compounds for use as pharmaceutical agence and in research settings. The present sequence is human endogenous orphan GPCR CDNA.
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                                                                                                                                                                                                                                                                           New human G protein-coupled receptor and its coding cDNA, useful for disease or disorder identification and/or selection, for screening of candidate compounds useful as pharmaceutical agents, and in research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCCTTGGCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 13; 53pp; English.
99US-0157282P.
99US-0157293P.
99US-0157294P.
99US-00417044.
2002US-00272983.
                                                                                                                                                                                           Liaw CW,
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                                                                                                     CHEN R.
DANG H T.
LIAW C W.
LIN I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cDNA encoding a non-endogenous, constitutively activated version of a human G protein-coupled receptor, useful for identifying receptor, inverse or partial agonists having potential applicability as therapeutic
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LOWITZ K.
CHALMERS D
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8.1 569 9 DA257272 8.1 499 7 BF567596 8.1 575 9 DA360011 7.5 1046 3 BQ950659 7.4 921 14 CNS03296 7.0 038 10 DV891040 6.9 754 3 BU468854 6.8 505 3 BU468854 6.8 556 7 AW654609	78.8 6.6 127 20 3 10 20 20 20 20 20 20 20 20 20 20 20 20 20	6.3 890 2 BIT31453 6.3 1946 6 AK156130 6.2 281 7 BB592940 ALIGNMENTS		Luuber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.  EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.) Unpublished (2003) Contact: MIPS MIPS MIPS Ingolsteacter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert	Clone t Researc sequenc consort No s1 This c1 Please Berlin-	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="DKFZp781C0629" /dab_host=="DH10B" /lab_host=="DH10B" /clone llb="781 (synonym: hlcc4)" /note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB;
	n n		BX64311 BX643113 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM	TITLE JOURNAL COMMENT	FEATURES BOULC	ORIGIN
GenCore version 5.1.8  Copyright (c) 1993 - 2006 Biocceleration Ltd.  OM nucleic - nucleic search, using sw model  Run on: May 22, 2006, 19:24:55 ; Search time 6433 Seconds (without alignments) (without alignments) (10222, 468 Millian cell undates)	US-10-626-445-5 score: 1176 table: lagtcggagtctaacagtacaccagtcagtatcttctga table: IDENTITY NUC Gapop 10.0, Gapext 1.0 d: 48236798 seqs, 27959665780 residues umber of hits satisfying chosen parameters: 96473596	DB seq length: 2000 DB seq length: 2000 Occessing: Minimum Ma Maximum Ma Listing fi EST:* 1: 9D-est1 2: 0b-est1	3: 9D-est1:* 4: 9D-est5:* 5: 9D-est2:* 7: 9D-est2:* 8: 9D-est7:* 9: 9D-est9:* 10: 9D-est9:* 11: 9D-9ss1:* 12: 9D-9ss2:* 14: 9D-9ss3:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES  Result  Ouery  No. Score Match Length DB ID	1 438.6 37.3 839 4 BX643713 BX	11.0 853 5 10.8 684 10 9.7 574 9 9.0 755 9 8.6 687 10 8.4 643 1 8.4 824 9

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podates by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5' ECORV-XmnI/Not1-3', E-S-CRON-XmnI/Not1-3', E-CRON-XmnI/Not1-3', For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTGGAT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
                                                                                                                                                                                           CDNA Library Preparation: GPCR Consortium CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL) DNA Sequencing by: The 1.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at: http://image.llnl.go.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAGCCTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TATGTCCTTAGTAGCTTTTGCTATAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCCTTGGCATTTTT
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                 Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="mixed"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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AGENCOURT_14740195 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:6971900 5', mRNA sequence.
                              Length 839;
                         Score 438.6; DB 4; Length
Pred. No. 3.8e-118;
0; Mismatches 174; Indels
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NIH-MGC http://mgc.nci.nih.gov/.
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75.9%;
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**ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT** TTAATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAGCCTTT

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241 AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA 300

262 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACGGCA

322 GCTGTATATAAGATTGTCCTCATCAGCTATGATAAATACCTGTCAATCTCAAATGCTTTG 381

rcrrargeaacecaaaaacecececereaaga 415

TCTTATAGGGCTCAACACACTGGCATCATGAAGA 394

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1. .721
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/clone=lib="VetCr: pcDNA3.1, Site 1: multiple, Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pcDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie webbite, using the Guthrie ID given in the fille
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a. Note: this is a NIH_MGC_Library."
                                                                                                                           475 TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCCATCACATC 534
                                                                                                                                                                                              603 GAGCCTGTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACTAC 662
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Concact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloAn? Bethesda, MD 20892
Email: cgapbs-r@mail.inh.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie CNA Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBIB row: a column: 04
High quality sequence start: 2
High quality sequence start: 2
High quality sequence stop: 328.
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1 (bases 1 to 721)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
663 CTCTTCCAGTGCTTCAGGACACTTACACAGAGCTGGGGGTGGCTTGCAGGA 712
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AGENCOURT 30842625 NIH_MGC_146 Homo sapiens cDNA clone
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normanlization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
                                                           Mus musculus adult male cortex cDNA, RIKEN full-length enriched library, clone:B530005H20 product:histamine receptor H 3, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High-efficiency full-length CDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                      AK140374 AK140374.1 GI:74150094
                                                                                                                                                                                                                                                                                                                                                                                                             HTC; CAP trapper
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21.9%; Score 25%; DB %; Length 721; 78.4%; Pred. No. 1.4e-64; ive 0; Mismatches 85; Indels

Query Match
Best Local Similarity 78.45
Matches 309; Conservative

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Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Balake,J., Boffelli,D., Bolunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Ring,B., Ringvald,M., Rodriguez,I., Sakamoto,N., Sasaaki,H.,
Saro,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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Nature 420 (6915), 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN Genome Exploration Research Group Phase II Team and the
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Ringwald, M. Roet, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Shenga, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, B., Sugiura, K., Sultana, R., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, B., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, B., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukude, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaij, H., Kawagashira, N., Kawashima, T., Kojima, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Plessy, C., Shibara, K., Shizaki, T., Suzuki, S., Tagami, M., Waki, K., PantoM Consortium landscape of the mammalian genome
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, TWB.:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and
Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M.
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/strain="C57BI/6J"
/db_xref="RANTOM_DB:B530005H20"
/db_xref="taxon:10090"
/clone="B530005H20"
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Best Local Similarity 59.1
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           /db xref="G1:71150095"
/translation="MGGMLIVAKVLGNALVMLAFVADSSLRTCHNFFLLNLAISDFLV
ARACTOHLYPYULTGRWFFGGLCKLWIVDVLLLCASSVFNTUTISYPRAVS
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ITASTLEFFTPPLSVTFPNLSIYLNIORRTRARLAGGGREAGPEPPDAQPSPPAPPS
CWGCWPKGGREAMPLHRYGVGRACPGFGCGGGGGGGGAASPFSSGSSRGTE
RPRSLKRGSKPSASSASLEKRMKWVSCSITCRIRLSRDKKVAKSLAIIVSIFGLCWAP
YTLLMITRAACHGHCVPDYWYETSFWLWANSAVNPULYPLCHYSFRRAFTKLLCPQX
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Koop, B. F. Davidson, W. S. and cGRASP Consortium.

Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
                                                                                                                                                                                                                                                                                                       CTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAGCCTTTGTGGTGGACAGAAACCT
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Salmo salar
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CB556920.1 GI:29496320
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Centrer for Blomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3NS, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
Sequenced by: Genome Sciences Centre, BC Cancer Agency F
Marra. Bioinformatics: Centre for Biomedical Research, 1
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Pred. No. 3.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                             of Victoria Jong Leong, BF Koop.
Insert Length: 791 Std Error: 0.00
Plate: 575
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High quality sequence stop: 791
Location/Qualifiers
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/lab_nost="NH10B"

/clone lib="NHH MGC 145"

/note="vector: pcDNA3.1; Site_1: varies by clone; Site_2:
/note="vector: pcDNA3.1; Site_1: varies by clone; or pcDNA3.1; Site_1: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRv-xmmI/Xhol-3', EcoRv (TA cloned, non-directional).

For information about which gene each clones represents, places out the variety our anonymous fip site at the properties of the properties of the properties of the site our anonymous fip site at anonymous and site at anonymous anonymous fip site at anonymous anonymous lands.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                1 (bases 1 to 732)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: GPCR Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBIO2 row: b column: 06
High quality sequence stop: 610.
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                                                                                                                                       Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPOR Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:6971899"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="mixed"
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AGENCOURT 14740187 NIH MGC_145 Homo sapiens cDNA clone
IMAGE:6971899 5', mRNA sequence.
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                                                                            Euteleostomi;
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                                                                                                                                                                              Amgen Rat ES: r.c.g.
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00001 row: d column: 6.
Location/Qualifiers
                                               Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
1 (bases I to 672)
Amgen EST Program.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="urgp1-00001-d6"
/clone="bb="urgp1 (14349)"
/note="Vector: pSPORT1; Rat GPCR library
internal pSPORT vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            598 gerecrecericergergrandegecergecarecreaginggal
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57.2%; Pred. No. 2.6e-28;
iive 0; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
                               Rattus norvegicus (Norway rat)
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CF147822.1 GI:33244090
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Homo sapiens
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195 182

Gaps

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셤 ઠે q ሯ 8 ò 셤 RESULT 8 DT257276

VERSION KEYWORDS SOURCE

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1 (bases 1 to 558)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Satico, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishidashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 CGCCACGGTTCTCGGGAAAGTTTTAGCTTTTTAGTGGTGGAAAAGTTTACG 375
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
                                                                                                                                                                                                           21 TGGCATCTTGCCACCAGCTGCTCAGGTCCCCTTGGCATTTTTAATGTCTTCATTTGCCTT
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Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
          Length 728;
     11.1%; Score 130.2; DB 10; Length 57.3%; Pred. No. 1.2e-26; Live 0; Mismatches 188; Indels
DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 AAAIGGCCCGAIGAITCIGGCTICAGA 464
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Contact: Takao Isogai
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                                                                                                               Conservative
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          Query Match
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CDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: BST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
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High quality sequence stop: 706.
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1 (bases 1 to 728)
Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C., Borsestoni, P. and Lindquist, E.A.

DoE Joint Genome Institute Pimephales promelas EST project Unpublished (2005)
Other ESTs: JGI CAAU8039.rev
Contact: Lindquist, E.A., Richardson, P.

DOE Joint Genome Institute
Contact: Lindquist, E.A., Richardson, P.

DOE Joint Genome Institute
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Fax: 925 296 5710
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Xenopodinae; Xenopus; Xenopus.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
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55.5%; Pred. No. 2.2e-26;
iive 0; Mismatches 228;
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                                                                                                                                                                                                                        /clone="BRHIP2025783"
/tissue type="hippocampus"
/clone_lib="BRHIP2"
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                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
                              pass sequencing: RAB.
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Salmo salar
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone lib="NICHD_XGC_EPTOR () Site 1: Not1;
/note="Organ: eye; Vector: pCWV-SPORT6; Site 1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC) library."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14564 row.f column: 24
High quality sequence stop: 707.
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EST ssal rgb2 40661 rgb2 Salmo salar cDNA clone
ssal rgb2_566_015_rev 5', mRNA sequence.
DW5762422
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58.7%; Pred. No. 2.6e-26;
iive 0; Mismatches 168;
                                           Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement:
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/organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6949081"
National Cancer Institute / NIH
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Best Local Similarity 58.7
Matches 243; Conservative
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Query Match
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Matches
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KEYWORDS
SOURCE
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                                                                                                                         Centre for Blomedical Research
University of Victoria
DO BOX 3020 STN CSC, Victoria BC, VBW 3N5, Canada
PO BOX 3020 STN CSC, Victoria BC, VBW 3N5, Canada
Fax: 250 472 4057
Fax: 250 472 4057
Email: bkoop@uvic.ca
Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M.
Marra. Bioinformatics: Centre for Biomedical Research, University
of Victoria Jong Leong, BF Koop.
Insert Length: 542 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AGAGGTCTCTGTAAGCTGTGGCTCCTCATGGACTACTTGCTCTGCACTGCCTCTGTTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Salmo salar"
/mol type="mRNA"
/strain="McConnel1"
/db xref="taxon:8030"
/clone="ssal rgp2_566 015 rev"
/tissue type="mixed tIssue"
/clone_lib="rgb2"
/note="Corgan: brain, kidney, spleen; Vector: pCMVsport6; ssalrgb2 mixed tissue Salmo salar cDNA; Tissue contributors: Robert Devlin (DFO, Vancouver, B.C.)"
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                      1 (bases 1 to 542)
Koop, P.F., Davidson, W.S. and cGRASP Consortium.
Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
Unpublished (2006)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 CCTGCCGACGAGTGTTTCGCTGAGTTCTACTGCACCTGGTACTTCCTACTCAGTGCGTCT
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Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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0; Mismatches 207; Indels
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Location/Qualifiers
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                                                                                                              Contact: Koop BF
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Sequencing
The British Columbia Cancer Agency Genome Science Centre
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6
Tel: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering.information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
Plate: 309 row: C column: 10
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bosinae; Bos Bosinae; Buterfield; Y., Xirkpertick, R., Liu, J., Guin, R., Chan, A., Buterfield; Y., Kirkpertick, R., Liu, J., Guin, R., Chan, Rathewson, C., Waye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., Ge Jong, P., McWilliam, S., Barris, W., Barra, M., Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398 Unpublished (2003) Other GSSS: CH240_309C10.TARBAC13P2
CC+81311 684 bp DNA linear GSS 16-JUN-2003 CH240 309C10.T7 CHORI-240 Bos taurus genomic clone CH240_309C10, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 TITATICATCCTCACAAGCTCTTCAACTGGGAGTTTGAAAAAAACATTTGTGTCTTTTG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 GCTCATTACTGACTATCTTTTGTGCACCGCATCTGTCTACAATATTGTCCTCATTAGCTA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 GCTCACTACTGACTATCTTTTGTGTACAGCATCTGTGTATAACATCGTACTCATCAGCTT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 racgiecrarariterraricarritrirritecececarecaestareareceatrice 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /call type="Blood"
/clone lib="CHORL-240"
/note="Wetcor: PTARBACI.3; Site 1: MboI; Site 2: MboI;
Hereford bull Li Domino 99375; CHORL-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAATTATTTTTTTTTTTTTTGGCTATTTCTGACTTCCTCGTGGGTTTGATTTCCATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.8%; Score 115.6; DB 1
70.6%; Pred. No. 2.6e-22;
ative 0; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_309C10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .684 /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                  CC481311.1 GI:31760574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                        Bos taurus (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                     CC481311
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us-10-626-445-5.rst

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Hominidae, Homo.

I (bases I to 755)

Kimura,K., Wakametu,A., Suzuki,Y., Ota,T., Nishikawa,T.,

Kimura,K., Wakametu,J., Sekine,M., Tsuriteni,K., Wakaguri,H.,

Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,

Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,

Murakwa,K., Ishidas,S., Ishibashi,T., Takahashi-Fujii,A.,

Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

Diversification of Transcriptional Modulation: Large-scale

Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="NT2RM2"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DA728518
DA728518 NT2RM2 Homo sapiens cDNA clone NT2RM2001941 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                316 gecarecridaderiadadanacerarecradadadadacerecranecreagadeceaegaeana 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 cerricercagedreacerrerrraacercageareraceacarecadades
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department o
Virology, Institute of Medical Science, University of Tokyo, and
HRI.
                                                                                                         256 CGGCGGGCAGTGCCGGAAGATGCTGCTGGTGTGGGTGCTGGCTTCCTGCTGCTACGGACCA
                                                                                                                                                                                       448 ATGATTCTGGCTTCAGA-----TTCTTGGAAGAACAGCACGAACACAAAGGACTGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                           376 gecgagricricracaacrigiracricereareacgecriceaeceregagricriraeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562 CCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTTACTGGAGCCTGTGGAAGCGTAGG
                                                                                                                                                                                                                                                                                                                                                      502 CCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACAATGCTCTTGGAATTCCTGCTT
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2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 755;
                                    388 ATGAAGATTGTTGCTCAAATGGTGGCTGTTTGGATACTGGCTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.0%; Score 106; DB 9;
55.0%; Pred. No. 1.9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM2001941"
/cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 16 (1), 55-65 (2006)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoters of Human Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
DA728518
DA728518.1 GI:81799719
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FLJ Project (HRI Team)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622 GCTCTCAG 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496 cgccrccc 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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COMMENT
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DA728518
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KEYWORDS
SOURCE
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Fax: 81-438-52-3986
Email: fij-cdna@nifty.com
MEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRL); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo.

I (bases I to 574)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Ishi, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
                                                                                                                                                                                                                                                                    DA306992 BRHIP2 Homo sapiens cDNa clone BRHIP2023706 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 crenarenaceraceraceracececrecacerenaceraceraceracerenacera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 IGGCICATTACTGACTATCTTTTGTGCACCGCATCTGTCTACAATATTGTCCTCATTAGC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 ridecticaractocárcia de circia de contra d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 TACGATCGATACCAGTCAGTTTCAAATGCTGTGTGTTTATAGGGCTCAACACACTGGCATC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 TACGACCGCTTCCTGTCGGTCACCCGAGCGGTCTCATACCGGGCCCAGCAGGGTGACACG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 AACTICTICCIGCICAACCICGCCAICTCCGACTICCICGICGGCGCCTICTGCAICCCA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AATTATTTTTTTTTCTTAGGCTATTTCTGACTTCCTCGTGGGTTTGATTTCCATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 CTGTACATCCCTCACGTGTTGTTTAAC---TGGAATTTTTGGAAGTGGAATCTGCATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
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/tissue type="hippocampus"
/clone_Tib="BRHIP2"
/note="Vector: pME18SFL3"
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Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

Office of Cancer Genomics

Office of Cancer Institute / NIH

Bldg. 31 RmloAOV Betheada, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                             175 ATTICTGACTICCICGIGGGITIGATITICCATICCICIGIACATCCCICACGIGITG---
                                                                                                              232 TTTAACTGGAATTTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTG
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
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AGENCOURT 63489140 NIH MGC 145 Homo sapiens CDNA clone IMAGE:8317348 5', mRNA sequence.
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US-09-165-543-33

US-08-985-090-4

US-09-162-1

US-09-162-1

US-09-991-053-13

US-09-999-016-17027

US-09-999-016-17027

US-09-9826-509-514

US-09-9826-509-514

US-09-166-199-1

US-09-543-679A-2590

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US-09-016-434-1313
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Sequence 1, Application US/09414010
GENERAL INPORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Haz, Thomas M.
APPLICANT: Monse, Kelley L.
APPLICANT: Monse, Kelley L.
APPLICANT: Wang, Shelby P.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CNOIO69
CURRENT APPLICATION NUMBER: US/09/414,010
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTING VET. 2.1
SEQ ID NO 1
LENGTH: 1173
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2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PPCTUS_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/PCCCMB.seq:*
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                      GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-891-053-26
US-09-165-543-4
US-09-165-543-4
US-09-165-543-3
US-09-165-543-3
US-09-642-514-6
US-09-642-514-6
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Sequence 1, Application US/09812216
Patent No. 6613533
GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Maz, Thomas M.
APPLICANT: Monsma, Frederick J. Jr.

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                                                                                                                                                                                                                                                                                           Score 686.6; DB 3;
Pred. No. 1.6e-201;
0; Mismatches 284;
             APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 1
                                                                                                                                                                                                                                                                                           sch 58.4%; al Similarity 75.1%; 886; Conservative
Umland, Shelby P.
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PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 74
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CORGANISM: Homo sapiens
US-09-875-076-13
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APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENO050
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 2001-06-06
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PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR PILLING DATE: 1999-02-16
PRIOR PILLING DATE: 1999-03-12
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PRIOR PILLING DATE: 1999-09-29
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APPLICANT: Nakamura, Takao
APPLICANT: Robayashi, Masahiko
APPLICANT: Tanaka, Masahiko
APPLICANT: Tanaka, Wasuka
APPLICANT: Tanaka, Yusuka
APPLICANT: Hidaka, Yusuka
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT APPLICATION NUMBER: PCT/JP99/07280
PRIOR PILING DATE: 1999-12-24
PRIOR PILING DATE: 1998-12-25
PRIOR PLING DATE: 1998-12-25
PRIOR PILING DATE: 1998-12-25
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version 4.0
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14.7%; Score 172.8; DB 3;
Best Local Similarity 49.6%; Pred. No. 9.9e-43;
Matches 562; Conservative 0; Mismatches 557;
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Patent No. 6750322
GENERAL INFORMATION:
APPLICANT: Itadani, Hiraku
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890 CAGTTCCCATCCCCGAGGCCACTGCTATGCTGAGTTCTTCTACAACTGGTACTTTCTCAT 949
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; Sequent No. 6093545
; GENERAL INFORMATION:
    APPLICANT:
    APPLICANT:
    APPLICANT:
    APPLICANT:
    ANDREW O.J. Goodearl and Sandra Glucksman
    TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
    NUMBER OF SEQUENCES: 39
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: LAHIVE & COCKFIELD, LLP
    STRET: 28 State Street
    CITY: Boston
    STATE: Massachusetts
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COMPUTER: IBM PC compatible
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
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PRICK APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
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ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanle
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                                                                                                                                                                                                                                                                                                             APPLICANT: Takimura, Tersuo
APPLICANT: Nakamura, Takao
APPLICANT: Nakamura, Takao
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Tanaka, Yusuke
APPLICANT: Hidaka, Yusuke
APPLICANT: Hidaka, Yusuke
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
TITLE OF INVENTION: NOVEL GUANOSINE
FILE REFERENCE: 06501-08301
CURRENT APPLICATION NUMBER: PCT/JP99/07280
PRIOR PILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-12-25
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 26
SSOFTHARE: FastSEQ for Windows Version 4.0
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                                                             Sequence 5, Application US/09891053
Patent No. 6750322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1). T. (2700)
OTHER INFORMATION: n = A,T,C or
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Best Local Similarity 49.6
Matches 562; Conservative
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NAME/KEY: CDS
LOCATION: (351)...(1589)
NAME/KEY: misc. feature
LOCATION: (1)...(2700)
                                                                                                                                                                                                                                                                    APPLICANT: Itadani, Hiraku
                                                                                                                                                                                                       GENERAL INFORMATION:
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LENGTH: 2700
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RECISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHRACTERISTICS:
LENGTH: 1338 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-165-543-6
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Sequence 26, Application US/09891053
Patent No. 6750322
GENERAL INFORMATION:
APPLICANT: Itadani, Hiraku
APPLICANT: Takimura, Tetsuo

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                                                                                                                  APPLICANT: Other, Masataka

TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)

TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)

TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS

FILE REFERENCE: 06501-083001

CURRENT FILING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: PCT/JP99/07280

PRIOR APPLICATION NUMBER: PCT/JP98/05967

PRIOR APPLICATION NUMBER: PCT/JP98/05967

PRIOR APPLICATION NUMBER: PCT/JP98/05967

PRIOR APPLICATION NUMBER: DT 1999-12-25

PRIOR APPLICATION NUMBER: DT 11145661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.2%; Score 143.2; DB 3; Length 3 Best Local Similarity 54.2%; Pred. No. 1.7e-33; Matches 339; Conservative 0; Mismatches 278; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
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Nakamura, Takao
Kobayashi, Masahiko
Tanaka, Ken-ichi
Hidaka, Yusuke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (302)...(1636)
US-09-891-053-26
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    GATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGA-----TTCTTGGAA 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08985090
Patent No. S885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1437 CATCTACCTGAACATCCAGAGGCGCA 1462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REGISTRATION NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD, STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STRANDEDNESS: single
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MOLECULE TYPE: CDNA
FEATURE:
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Best Local Similarity
Matches 341; Conserv
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US-08-985-090-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 CTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCACGTGTTTTAAC---TG 239
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                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.2%; Score 143.2; DB 3; Best Local Similarity 54.2%; Pred. No. 2.2e-33; Matches 339; Conservative 0; Mismatches 278;
CATCTACCTGAACATCCAGAGGCGCA 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                 E: LAHIVE & COCKFIELD, LLP
28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
                                                                                                              Sequence 4, Application US/09165543
Patent No. 6093545
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3244 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                      Massachusetts
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CITY: Boston
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                                                                                                                                                                                                                                                                                    ADDRESSEE:
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; LOCATION:
US-09-165-543-4
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  594 GATTTACTGGAGCCTGTGGAAGCGTAGGGCTCTCAG 629
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NIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
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                                                    NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFRENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617)227-7400
TELEFRAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 135,5 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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; Sequence 6, Application US/09167354A

; Patent No. 613659

; GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
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US-09-165-543-3
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TYPE: DNA ORGANISM: Artificial Sequence
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53.6%; Pred. No. 1.1e-32;
tive 0; Mismatches 286; Indels 9;
APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: Pyati, Jayashree
APPLICANT: Pyati, Jayashree
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF 'ITLE OF INVENTION: SUBTYPE
FILE REPERENCE: JW
CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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Sequence 6, Application US/09642855 Patent No. 6413743 GENERAL INFORMATION:

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APPLICANT: Pyati, Jayashree
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APPLICANT: Huvar, Arne
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/642,855
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 09/167,354
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
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US-09-642-514-6
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                                                                                                                   APPLICANT: Pyati, Jayabhree
APPLICANT: Pyati, Jayabhree
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DUA ENCODING A HUMAN HISTAMINE RECEPTOR (
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: ORT1290
CURRENT APPLICATION UNMBER: US/09/642,514
PRIOR APPLICATION NUMBER: US 09/167,354
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 1998-10-06
SOFTWARE: PATENTIN NOS: 8
SOFTWARE: PATENTIN VOY: 2.0
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APPLICANT: Extander, Mark
APPLICANT: Extander, Mark
APPLICANT: Huvar, Anne
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/642,852
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 09/167,354
PRIOR APPLICATION NUMBER: 09/167,354
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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                              Sequence 21, Application US/09891053
Fatent No. 675032
GENERAL INPORMATION:
APPLICANT: Itadani, Hiraku
APPLICANT: Tadani, Hiraku
APPLICANT: Tadani, Masahiko
APPLICANT: Robayashi, Masahiko
APPLICANT: Robayashi, Masahiko
APPLICANT: Robayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yusuke
APPLICANT: Ohta, Masataka
ITILE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
ITILE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
ITILE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: PCT/JP99/07280
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-12-25
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SEO IN NO. 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (271)...(1629)
US-09-891-053-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
RESULT 15
JS-09-891-053-21
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LENGTH: 2050
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Search completed: May 22, 2006, 21:34:40 Job time : 267 secs

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ORGANISM: Mus musculus
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| FEMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/US108_PUBCOMB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/US118_PUBCOMB.seq:*
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Sequence 14, Appli
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                                                                                                         May 22, 2006, 21:13:09 ; Search time 1522 Seconds (without alignments) 9494.257 Million cell updates/sec
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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0 US-10-626-398-6

US-09-812-216-1

US-09-910-411-1

US-09-976-25-13

US-09-876-25-13

US-09-876-25-13

US-10-052-193-1

US-10-052-193-1

US-10-354-059-1

US-10-354-059-1
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US-10-349-253A-1
US-10-723-955-13
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Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DAME Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0032
CURRENT APPLICATION NUMBER: US/10/626,445
CURRENT FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: 09/790,849
PRIOR PILING DATE: 2001-02-22
PRIOR PLING DATE: 2000-05-31
PRIOR PLING DATE: 2000-05-31
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
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                            US-10-616-088-1

US-10-626-126-1

US-10-723-955-13

US-09-891-138A-5

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US-09-891-138A-628

US-10-225-165-1

US-10-225-165-1

US-10-284-206-19

US-10-684-206-19

US-10-290-078-26

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US-10-290-078-26

US-10-290-078-26

US-10-290-078-26

US-10-488-421-5

US-10-626-445-7

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US-11-241-956-19
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US-10-759-463-2
US-09-891-053-5
US-10-759-463-5
                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5, Application US/10626445; Publication No. US20040248252A1; GENERAL INFORMATION:
                                                                                   8888
9077
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APPLICANT: Lovenberg, Timothy
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Sequence 5, Application US/10626126 Publication No. US20050074770A1 GENERAL INFORMATION:

US-10-626-126-5

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APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0033
FURRENT APPLICATION NUMBER: US/10/626,126
CURRENT FILING DATE: 2003-07-23
FRIOR APPLICATION NUMBER: 09/790,849
FRIOR APPLICATION NUMBER: 60/208,260
FRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
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ATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGTTCC	) [][	AGGAAGCTAGCCAGGCCATCCTTCTGAGGCGCTTTTGCCATTTGCTGGGCTCCAAGGCTCCAAGGCTCCAAGGCTTTTGCTGGGCTCCAAGGCTCCAAGGCTTTTGCTGGGGCTCCAAGGCTCCAAGGCTTTTGCTGGGGCTCCAAGGCTCCAAGGCTTTTGCTGGGGCTCCAAGGCTTTTGCTGGGGCTTCAAGGCTCCAAGGCTTTTGCTTGC		TIGHTACAGCATTCCCTTTCAACTTACCCCCCCCCCCCCCCC		CCAGCGCTGTCACAGAGATCAGTCTTCTTGA 1176	491191191919494949494949494949494949494	#626.398	FLICANT: LOVENDERGY, ITMOCHY PLICANT: LOVENDERGY, ITMOCHY TLE OF INVENTION: DNAB Encoding Mammalian Histamine Receptor Of The H4 Subtype LE REFERENCE: PRD-0034	RRENT FILING DATE: 2003-07-23 IOR APPLICATION NUMBER: 09/790, 849 IOR FILING DATE: 2001-02-22	INCH AFFILIATION NUMBERS: 0/208,200  IOR FILING DATE: 2000-05-31  MBER OF SEQ ID NOS: 27  TO NO PERSON 3.2	1D NO 5 ENCTH: 1176 YPE: DNA 1 RGANISM: Mus musculus	100.0%; Score 1176; DB 10; Length 1176; milarity 100.0%; Pred. No. 0; Conserving 0. Minarches 0. Tadels 0.	CTAACAGTACTGGCATCTTGCCACCAGTGCTCAGGTCCCCTTGGCATTT 60		121 GTGGTGGACAGAAACCTTAGACATCGAAGTAATTTTTTTT

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88.4%; Pred. No. 7.4e-291;
                CURRENT APPLICATION NUMBER: US/10/626,445
CURRENT FILING DATE: 2003-07-23
                     PRIOR APPLICATION NUMBER: 09/790, 849
PRIOR FILING DATE: 2003-07-23
PRIOR FILING DATE: 2001-02-22
PRIOR PILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
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 FILE REFERENCE: PRD-0032
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Pred. No. 7.4e-291;
0; Mismatches 136; Indels
PRIOR APPLICATION NUMBER: 09/790,849
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/208,260
PRIOR FILING DATE: 2000-05-31
NUMBER: OF SEQ ID NOS: 27
SOFFWARE: PatentIn version 3.2
SEQ ID NO 6
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Publication No. US20050074841A1
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The FILE FEFERENCE: PRO-0034
CURRENT APPLICATION NUMBER: US/10/626,398
CURRENT FILING DATE: 2003-07-23
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; Parent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Britzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michary Bavid
; APPLICANT: Michary Bavid
; APPLICANT: APPLICANT: APPLICANT: This and the sequence of the sequenc
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Patent No. US20020098539A1
GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Hackrick, Joseph A.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Wang, Suke
TILLE OF INVENTION: Histamine receptor
FILE REPERENCE: CN01069
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 1999-10-07
NUMBER: OF SECOLE NOSE: 8
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; Sequence 13, Application US/09875076; Publication No. US20030017528A1; GENERAL INFORMATION:
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Pred. No. 4.7e-205;
0; Mismatches 284;
              CURRENT APPLICATION NUMBER: US/09/910,411
CURRENT FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-02-03
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 1999-11-02
NUMBER: OF SEQ ID NOS: 2
SEQ ID NO 1
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Best Local Similarity 75.1%;
Matches 886; Conservative
REFERENCE: GP70655-2C1
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CORGANISM: Homo sapien
US-09-910-411-1
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                                                                 AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTTGCCATTTGCTGGGCTCCA
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781 ATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGTTCC
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
FILE REFERENCE: ARENOSO
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR APPLICATION NUMBER: 60/136,439
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PRIOR APPLICATION NUMBER: 60/136,439
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,653
PRIOR FILING DATE: 1999-05-29
PRIOR FILING DATE: 1999-09-29
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APPLICANT: Lin, I-Lin
APPLICANT: Lin, I-Lin
APPLICANT: Lin, I-Lin
APPLICANT: Lin, I-Lin
APPLICANT: Lina, Ruoping T.
APPLICANT: Lina, Chen W.
APPLICANT: Lina, Chen W.
TITLE REPRESENCE: RENEWORS TO THE REPRESENCE: AREN-0054
CURRENT APPLICANTION: NON-Endogenous Constitively Activated Human G Protein Coupled RF FILE REFERENCE: AREN-0054
CURRENT APPLICANTION NUMBER: 00/416,760
PRIOR APPLICANTION NUMBER: 00/170,496
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICANTON NUMBER: 60/12,946
PRIOR FILING DATE: 1999-03-12
PRIOR PRILING DATE: 1999-03-12
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835 Tricricciaaricadarrengradericricaccaaadadedaacargradaacreerradadee
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Publication No. US20030018182A1
GENERAL INFORMATION:
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APPLICANT: Lehmann-Bruinsma, Ka
APPLICANT: Chalmers, Derek T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lin, 1-Lin
APPLICANT: Dang, Huong T.
APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
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                            PRIOR APPLICATION NUMBER: 60/157,280
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR APPLICATION NUMBER: 60/157,281
PRIOR FILING DATE: 1999-10-01
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NUMBER OF SEQ ID NOS: 74
SOFTWARE: PARCHIN Ver: 2.1
        FILING DATE: 1999-09-29
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Best Local Similarity 75.1<sup>3</sup>
Matches 886; Conservative
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LENGTH: 1173
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                                                                                  121 GTGCTGGCCTTCTTAGTGATGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGA---- 476
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361 TCTTATAGAACTCAACATACTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420
                                                                                                                                                                                                                                                                                                  535 TCATTCTTGGAATTCGTGATCCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
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                                                                                                                                                                            477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGAATGGTACATCCTTGCCATCAC
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; Publication No. US20020132755A1
; GENERAL INPORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; CURRENT APPLICATION UNMER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; PRIOR FILING DATE: 201-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
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Pred. No. 4.7e-205;
0; Mismatches 284; Indels
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PRIOR FILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-09-29
PRIOR PLING DATE: 1999-10-01
PRIOR PRIOR APPLICATION NUMBER: 60/157,281
PRIOR PRING DATE: 1999-10-01
PRIOR PLING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 13
PRIOR PLING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 13
                                           R FILING DATE: 1999-08-27

R APPLICATION NUMBER: 60/108,029

R FILING DATE: 1998-11-12

R APPLICATION NUMBER: 60/136,436

R APPLICATION TOWER: 60/136,436

R APPLICATION NUMBER: 60/136,439
                                                                                                                                                                                           R FILING DATE: 1999-05-28
R FILING DATE: 1999-05-28
R FILING DATE: 1999-05-28
R APPLICATION NUMBER: 60/137,127
R FILING DATE: 1999-05-28
R PAPLICATION NUMBER: 60/137,131
R FILING DATE: 1999-05-28
R APPLICATION NUMBER: 60/137,131
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-06-29
APPLICATION NUMBER: 60/136,437
FILING DATE: 1999-05-28
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75.1%;
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Best Local Similarity 75.1
Matches 886; Conservative
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NUMBER OF SEQ ID NOS: 74
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, 1-Lin
APPLICANT: L
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CURRENT FILING DATE: 2002-10-17
PRIOR PELING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-0-12
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/121,946
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-05-28
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PRIOR PRIOR DATE: 1999-05-28
PRIOR PRILING DATE: 1999-05-28
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APPLICANT: Pfizer Inc.
APPLICANT: O'Reilly, Mark A.
APPLICANT: Peter, Beate
TITLE OF INVENTION: NOVEL POLYPEPTIDE
FILE REFERENCE: PC10373B
CURRENT APPLICATION NUMBER: US/10/354,769
CURRENT APPLICATION NUMBER: US 09/699,801
PRIOR APPLICATION NUMBER: US 09/699,801
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
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PRIOR FILING DATE: 1999-10-29
PRIOR PILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PARCHILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 10
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US-10-354-769-1
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Sequence 1, Application US/10354769 Publication No. US20030149242A1 GENERAL INFORMATION:

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961 TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG 1020
                                                                                                     Score 686.6; DB 7;
Pred. No. 4.7e-205;
0; Mismatches 284;
                                                                                                          58.4%;
75.1%;
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Matches 886; Conservative
                          ORGANISM: Homo sapiens
                                                    US-10-393-807-13
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CURRENT FILING DATE: 2003-03-21
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Publication No. US20030175891A1
GENERAL INFORMATION:
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
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APPLICANT: LAW. CAGN
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Dominic P.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION NUMBER: 09/10,496
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-11-27
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR PELICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-03-12-26
PRIOR PELICATION NUMBER: 60/123,945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/10417820A Publication No. US20030229216A1 GENERAL INFORMATION: Rupping APPLICANT: Chen, Rupping APPLICANT: Liaw, Chen W.
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GARBEAL INCOMPAULION:

GARBEAL INCOMPAULION:

APPLICANT: Healy, Aileen

TITLE OF INVENTION: Methods and Compositions for Treating

TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,

TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 14717, 9941, 19310, c

TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 14717, 9941, 19310, c

TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 14717, 9941, 19310, c

TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 14717, 9941, 19310, c

TITLE OF INVENTION WIMBER: US/11/242,505A

CURRENT FILING DATE: 2002-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-12-16

PRIOR FILING DATE: 2001-12-16

PRIOR FILING DATE: 2001-12-17

PRIOR FILING DATE: 2001-12-17

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSEQ for Windows Version 4.0

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Pred. No. 2.9e-209;
0; Mismatches 285;
US-11-242-505A-26; Sequence 26, Application US/11242505A; Publication No. US20060099656A1; GENERAL INFORMATION:
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APPLICANT: Garroll, Joseph M.
APPLICANT: Garroll, Joseph M.
APPLICANT: Healy, Aileen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 14717, 9941, 19310,
TITLE OF INVENTION: Hematological Disorders Using 252, 304, 1980, 14717, 9941, 19310,
TITLE OF INVENTION: Hematological Disorders Using 205-10-03
FILE REFERENCE: MPIZORION NUMBER: US/11/242,505A
CURRENT FILING DATE: 2002-11-07
PRIOR PILING DATE: 2002-11-07
PRIOR PAPLICATION NUMBER: US 60/347,949
PRIOR PILING DATE: 2002-12-16
PRIOR PILING DATE: 2002-12-16
PRIOR FILING DATE: 2002-12-16
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 1265

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GENERAL INFORMATION:

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                                                                                                           Score 685; DB 7; L
Pred, No. 3.1e-209;
0; Mismatches 285;
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Best Local Similarity 75.1%;
Matches 885; Conservative 0
                                 ORGANISM: Homo Sapiens
                                        ; ORGANISM: HOM
US-11-242-505A-25
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Sequence 25, Application US/11242505A Publication No. US20060099656A1

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 TGGTAGGCAATGCTGTGGTCATCTTAGCCTTTGTGGTGGACAAAACCTTAGACATCGAA 148
                                    623 TTGCTGGCAATGTGTGTCGTCTGTCTGCCGTGGGCTTGAACCGCCGGCTCCGCAACCTGA 682
                                                                                                                                                                                                                                              TCTACACCAGCCTGGATGTGATGCTCTGCACAGCCTCCATTCTTAACCTCTTCATGATCA 862
                                                                       GTAATTATTTTTTTTTTTTGGCTATTTCTGACTTCCTCGTGGGTTTGATTTCCATTC
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APPLICANT: Millennium Pharmaceuticals, Inc.
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; Sequence 23, Application US/11312958
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661 ACCTCTTCCAGTGCTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT
                                709 GTCTCTTCCAACATCTGTGGACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT
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APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND MONITORING TRANSPLANT REJECTION
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: SOG12000104
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR PILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
LENGTH: 1847
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APPLICANT: Wohlgemuth, Jav
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Publication No. US20060088836A1
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## APPLICANT: Millennium Pharmaceulicals, Inc.
### APPLICANT: Millennium Pharmaceulicals, Inc.
#### APPLICANT: Millennium Pharmaceulicals, Inc.
#### APPLICANT: Venkateswarlu, Karicheti
#### APPLICANT: Venkateswarlu, Karicheti
#### APPLICANT: Venkateswarlu, Karicheti
#### APPLICANT: Venkateswarlu, Karicheti
#### APPLICANTON: MENCOSIOAL DISORDERS USING 1455, 559, 34021, 44099, 25278,
#### TITLE OF INVENTION: 41260, 26099, 21407, 42032, 46656, 62853, 302, 333,
#### TITLE OF INVENTION: 41260, 26099, 21407, 42032, 46656, 62853, 302, 333,
#### TITLE OF INVENTION: 41260, 2012PIRNM OWNI
### CURRENT FILING DATE: 2003-01-16
### PRIOR FILING DATE: 2003-01-16
### PRIOR FILING DATE: 2003-01-18
### PRIOR FILING DATE: 2002-02-18
### PRIOR FILING DATE: 2002-02-18
### PRIOR FILING DATE: 2002-03-15
### PRIOR FILING DATE: 2002-04-19
### PRIOR PELING DATE: 2002-04-19
### PRIOR PELING DATE: 2002-04-19
### PRIOR APPLICATION NUMBER: US 60/414,262
### PRIOR APPLICATION NUMBER: US 60/414,262
### PRIOR APPLICATION NUMBER: US 60/419,986
### PRIOR PELING DATE: 2002-11-05
### PRIOR PELING DATE: 2002-05
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331 AGGGCTCCATCCTCAACCTCTGCCTCAGCCTGGACGGCTACCTG 378
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Bedilican No. US2006009594A1
GENERAL INFORMATION:
APPLICANT: NAGOYA INDUSTRIAL SCIENCE RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/11302678 Publication No. US20060088881A1 GENERAL INFORMATION:
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LOCATION: (468)...(1790)
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LENGTH: 1984
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Publication No. US2006008881A1
GENERAL INFORMATION:
APPLICANT: Milennium Pharmaccuticals, Inc.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Venkateswarlu, Karicheti
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: URGLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: MPIO2-012PIRMM OWNI
CURRENT APPLICATION NUMBER: US/11/302,678
CURRENT APPLICATION NUMBER: US/11/302,678
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                                                                          89 TGGTAGGCAATGCTGTGGTCATCTTAGCCTTTGTGGTGGACAAAACCTTAGACATCGAA 148
                                                                                                                                                                                  176 TCGTGGGCAACCTCCTGGTGATCCTCTCCGTGCTCAGGAACCGCAAGCTCCGGAACGCAG 235
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3.0%; Score 35.2; DB 7; Length 1323;
Best Local Similarity 54.8%; Pred. No. 0.11;
Matches 92; Conservative 0; Mismatches 73; Indels 3;
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PRIOR PILING DATE: 2003-01-16
PRIOR PLING DATE: 2003-01-16
PRIOR PLING DATE: 2003-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-01-18
PRIOR PLING DATE: 2002-03-15
PRIOR PLING DATE: 2002-03-15
PRIOR PLING DATE: 2002-03-15
PRIOR PLING DATE: 2002-03-15
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-09-27
PRIOR PLING DATE: 2002-10-21
PRIOR PLING DATE: 2002-10-21
PRIOR PLING DATE: 2002-11-05
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ORGANISM: Homo Sapiens
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US-11-302-678-42
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Sequence 3, Application US/10506549;
Publication No. US20060100417A1
GENERAL INFORMATION:
APPLICANT: APPLERA CORPORATION
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO01361-US
CURRENT APPLICATION NUMBER: US/10/506,549
CURRENT FILING DATE: 2004-09-03
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 394191
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; APPLICANT: GIFU INTERNATIONAL INSTITUTE OF BIOTECHNOLOGY
; APPLICANT: YAMADA, Yoshiji
; APPLICANT: YOKOTA, Mitsuhiro
; TITLE OF INVENTION. Method for diagnosing a risk of hypertension
; FILE REFERENCE: C0200701
; CURRENT APPLICATION NUMBER: US/10/528,659
; CURRENT FILING DATE: 2005-03-22
; PRIOR APPLICATION NUMBER: JP P2002-280034
; RIOR PILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
LENGTH: 50000
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 6; Length 50000;
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0; Mismatches 140; Indels
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, OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3
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Best Local Similarity 48.0%;
Matches 132; Conservative C
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US-10-528-659-2
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1678 TTTGCCATATTGATAGGCTCACTTGTTGTTGGAATAGCTGTTGTAGAGCACTACCCAACA 1737
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                                                                                                       Sequence 3, Application US/11317983
; Sequence 3, Application US/11317983
; Publication No. US2006009022A1
; GENERAL INFORMATION:
; APPLICANT: Zou, Jûtao
; APPLICANT: Taylor, David C
; APPLICANT: Wei, Yangdou
; APPLICANT: Jako, Colette C
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
; CURRENT PLLING DATE: 2005-12-23
; CURRENT PLLING DATE: 2005-12-23
; PRIOR PLLING DATE: 2005-04-28
; PRIOR FILING DATE: 2005-04-28
; PRIOR FILING DATE: 2005-03-29
; PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: FUJIWIRA, TOWOKO
APPLICANT: FUJIWIRA, TOWOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT FILING DATE: 2005-09-02
PRIOR PILING DATE: 2005-09-02
PRIOR PILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PATENTIN VERSION 3.3
SOFTWARE: PATENTIN VERSION 3.3
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Publication No. US20060099612A1
GENERAL INFORMATION:
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APPLICANT: Zou, Jitao

APPLICANT: Taylor, David C

APPLICANT: Taylor, David C

APPLICANT: Wei, Yangdou C

APPLICANT: Wei, Yangdou C

APPLICANT: Jako, Colette C

TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants

FILE REFERENCE: 3015-5684.1US

CURRENT APPLICATION NUMBER: US/11/317,983

CURRENT FILING DATE: 2005-12-23

PRIOR PILING DATE: 2005-04-28

PRIOR PLICATION NUMBER: 0S/11/117,005

PRIOR FILING DATE: 2001-03-29

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 1999-12-16

PRIOR FILING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PATENTIN VET. 2.1

SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                      Gaps
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nilarity 58.4%; Pred. No. 0.73;
Conservative 0; Mismatchec
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PRIOR APPLICATION NUMBER: 60/112,812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/11317983
Publication No. US20060090222A1
GENERAL INFORMATION:
                                                                                                                                            ; ORGANISM: Arabidopsis thaliana
US-11-317-983-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Arabidopsis thaliana
US-11-317-983-24
                                                                                                                                                                                                                          Query Match 2.9%;
Best Local Similarity 58.4%;
Matches 59; Conservative
                PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 5193
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nes 59; Conserv
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                                                                                                                                     TYPE: DNA
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APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: Silos-Santiago, Inmaculada APPLICANT: Venkateswarlu, Karicheti

Sequence 21, Application US/11302678 Publication No. US20060088881A1 GENERAL INFORMATION:

US-11-302-678-21

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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLOGICAL DISCREBES USING 1435, 559, 44029, 25278,
TITLE OF INVENTION: 12303, 985, 1327, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: MPIO2-012PIRMM OWNI
CURRENT APPLICATION NUMBER: US/10/345,680
PRIOR APPLICATION NUMBER: US 60/349,511
PRIOR APPLICATION NUMBER: US 60/360,500
PRIOR APPLICATION NUMBER: US 60/365,041
PRIOR APPLICATION NUMBER: US 60/365,041
PRIOR PILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-03-16
PRIOR APPLICATION NUMBER: US 60/403,468
PRIOR FILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US 60/419,986
PRIOR APPLICATION NUMBER: US 60/423,809
PRIOR APPLICATION NUMBER: US 60/429,797
PRIOR PILING DATE: 2002-11-05
PRIOR PILING DATE: 2002-10-07
PRIOR PILING DATE: 2002-11-05
PRIOR PILING DATE: 2002-10-07
PRIOR PILING DATE: 2002-10-07
PRIOR PILING DATE: 2002-10-07
PRIOR PILING DATE: 2002-10-07
PRIOR PILING DATE: 2002-11-05
PRIOR PILING 
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; Publication No. US2006008881A1
; GENERAL INFORMATION:
   APPLICANT: Millennium Pharmaceuticals, Inc.
   APPLICANT: Silos-Santiago, Inmaculada
   APPLICANT: Venkateswartlu, Karicheti
   APPLICANT: Venkateswartlu, Karicheti
   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
   TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Best Local Similarity 45.2%;
Matches 123; Conservative
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ORGANISM: Homo Sapiens
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US-11-302-678-21
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34021, 44099, 25278,
62553, 302, 323,
2058 OR 6351 MOLECULES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 TCATCTGATTGCTTGTTGATAATGTCTGCCTTTTCAATAGCGCCATTTTTGCTCTTC
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APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: Verkateswarlu, Karicheti
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 3402
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2056
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2056
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2056
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2056
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2056
TITLE OF INVENTION: NUMBER: US 60/360,500
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/374,063
PRIOR FILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 66
NUMBER OF SEQ ID NOS: 66
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33.4; DB 7;
Pred. No. 0.16;
0; Mismatches 96;
                    FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
FRIOR APPLICATION NUMBER: US 10/932,182
FRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81301
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Publication No. US20060088881A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.8%;
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Best Local Similarity 48.7
Matches 91; Conservative
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## TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323, TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.

### FILE REPERENCE: MPIOL-012PIRM OWNI
CURRENT APPLICATION NUMBER: US/11/302,678

### CURRENT FILING DATE: 2005-12-14

### PRIOR PELING DATE: 2003-01-16

### PRIOR FILING DATE: 2002-01-18

### PRIOR FILING DATE: 2002-01-8

### PRIOR PELING DATE: 2002-02-8

### PRIOR PELING DATE: 2002-03-8

### PRIOR FILING DATE: 2002-03-8

### PRIOR PELING DATE: 2002-03-15

### PRIOR PELING DATE: 2002-09-27
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Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAWURA, YOKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YOKIKO
APPLICANT: RUJNURA, TOWOKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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Pred. No. 0.33;
0; Mismatches 149; Indels
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PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/423,809
PRIOR PILING DATE: 2002-11-05
PRIOR PLICATION NUMBER: US 60/429,797
PRIOR FILING DATE: 2002-11-26
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 45.2%;
Matches 123; Conservative
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US-11-302-678-19
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ORGANISM: Homo Sapiens
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NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 19
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1040 GGCTGCAATGGTTCAATTCGTTTGTTAATCCCTTTCTGTACCCTTTGTGTCACGGCGTT 1099
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                                                                                                                                               920 TCAGTCCCTCTGCTCCTGTGACATCCCCGCCA-----TCTGGAAAAGCATCTTCCTGT 973
                                                                                                                                                              Query Match 2.8%; Score 33.4; DB 7; Length 1074; Best Local Similarity 50.7%; Pred. No. 0.36; Matches 110; Conservative 0; Mismatches 101; Indels 6; Gaps
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Search completed: May 22, 2006, 21:35:40 Job time : 26 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

May 24, 2006, 13:31:49 ; Search time 195 Seconds (without alignments) 916.778 Million cell updates/sec

US-10-626-445-8 Perfect score: ritle:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 seqs, 457216429 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp1990s:\* Genesed •• Database

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2004s:\* geneseqp2005s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:\*

## SUMMARIES

	3 ID Description	5 AAM50565 Aouse his	8 ADO29497 Ado29497 Mouse GPC	5 AAM50566 Rat hista	3 AAB02831 Human G p	3 AAY71297 Auman or	4 AAB62445 Human GPC	4 AAG64477 Human G	Human G	Human	Human	ABB78276 Amino	5 AAM50564 Human his	5 AAG66023 Auman his	Amino	ABG71960 Human	Human	6 ABP81727 Human his	AAE36417	7 ADG98760 Adg98760 Human orp	7 ADJ26923 Auman end	ADG86375	8 ADJ88376 Adj88376 Novel hum	
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æ	uery	99.4	99.4	85.2	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	6.99	
	Scor	2035	2035	1745	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	1370.5	
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Ado29496 Human GPC Adp20168 Human G p Adq75074 Human G p Ady86900 Human his	Aam53052 Human G p Aam53053 Human G p Aam51410 Human GPR Aae36416 Human H4		Aae36414 Human H4 Adu82861 Ligand up Aac02530 Human H3 Aaw92975 Human mAC Aav06322 Human G D	
ADO29496 ADP20168 ADQ75074 ADY86900	AAM53052 AAM53053 AAM51410 AAR346416	ADG86522 AAM50567 AAE36415	AAE36414 ADU82861 AAO29530 AAW92975 AAY06322	AAG67830 AAY92218 AAB30627 ABB79792 ABR43667 ABF57425
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	391 5	390 8 389 8	336 649 649 445 7	444444 444444 725222 72645
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## ALIGNMENTS

RESULT

AAM50565 standard; protein; 391 AA Mouse histamine H4 receptor. (first entry) 18-MAR-2002 AAM50565; AAM50565 

Histamine H4 receptor, mouse, antiasthmatic, antiallergenic, antiinflammatory, cardiant, circulatory, antidiabetic, laxative, diagnosis; gene therapy.

Mus musculus.

WO200192485-A1.

06-DEC-2001.

22-FEB-2001; 2001WO-US005914.

31-MAY-2000; 2000US-0208260P.

(ORTH ) ORTHO-MCNEIL PHARM INC.

Lovenberg T, Liu C;

WPI; 2002-114339/15. N-PSDB; AAI70981.

New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.

Claim 13; Fig 5B; 92pp; English.

The present sequence is that of a mouse histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a spleen cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4

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receptor activity. Recombinant protein is useful for identifying modulators of the histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
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0
                                                                                                                                                                                  Length 391;
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                                                                                                                                                                                Score 2035; DB 5;
Pred. No. 8.2e-202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 PLCHRRFQKAFWKILCVTKQPALSQNQSVSS 391
                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                  99.4%;
                                                                                                                                                                              Query Match
Best Local Similarity 99.7
Matches 390; Conservative
                                                                                                                                            Sequence 391 AA;
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indentify disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; nutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; covary disorder; uterus disorder; prostate disorder; testis disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cytostatic; antinflammatory; vasotropic; antianginal; antiarrhythmic; CNS; central nervous system; respiratory; antidiarrhoseic; antidiaberic; virucide; hepatotropic; antibrocerial; antidiaberic; dermacological; antiulcer; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
                                                                                                                                                                                                                G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder;
                                        AD029497 standard; protein; 391 AA.
                                                                                                                                                                          Mouse GPCR HRH4, SEQ ID NO:599
                                                                                                                                 29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   murine; receptor
                                                                                      AD029497;
RESULT 2
                    AD029497
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WO2004040000-A2 13-MAY-2004

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The invention relates to human and mouse G protein-coupled receptors

(GPCRs) and nucleic acids encoding them. The invention also relates to
sequences at least 90% identical to the GPCR proteins and nucleic acids
of the invention; methods of treating, preventing or diagnosing diseases
associated with GPCRs of the invention; methods of screening for
compounds useful in the treatment of GPCR related diseases, a transgenic
compounds useful in the treatment of GPCR related diseases, a transgenic
mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
from the trasngenic mice; kits comprising several mice each of which has
comprising a GPCR transgene or in an endogenous GPCR gene; cells derived
from the trasngenic mice; kits comprising several mice each of which has
comprising a GPCR nucleic acid. The GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR polypeptides and vectors
comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
be used in the diagnosis, treatment or prevention of a wide variety of
diseases including neurological disorders (e.g., Alzheimer's disease,
disperders of the adrenal gland; disorders (e.g., Alzheimer's disease,
disorders of the adrenal gland; disorders (e.g., auciment);
compounders (e.g., auciment);
anaemia or leukaemia); immune disorders (e.g., aucimented archythmia or
ADDS; bone and joint disorders (e.g., aucimented disorders or
ADDS; bone and joint disorders (e.g., aucimented archythmia or
comprising sour or osteoporosis); methodic or nutritive disorders (e.g.,
anaemia or leukaemia); immune disorders (e.g., aucimented archythmia or
comprising disorders of the kidney, liver, lung, breast, ovary,
obesity, enzyme deficiency-related diseases or vitamin deficiency-related
comprision of the printed specification; those sequences not shown were obtained in
compression of the printed specification; those sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240
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                                                                                                                                                                                                                                                                                                      Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
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Zeng H;
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                                                                                                                                                                        3A, Bergmann JE, Gragerov A, Hohmann J,
Mcilwain KL, Pavlova MN, Vassilatis D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2035; DB 8;
Pred. No. 8.2e-202;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 151; SEQ ID NO 599; 542pp; English
                                                                                                                                                                                                                                                                                                                                                                            pectoris, Parkinson's disease.
                  09-SEP-2003; 2003WO-US028226.
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                                                               09-SEP-2002; 2002US-0409303P.
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Best Local Similarity 99.7
Matches 390; Conservative
                                                                                                                                                                                                                                          WPI; 2004-390329/36.
                                                                                                                               (PRIM-) PRIMAL INC
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                                                                                                         301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.
                                                             300
                                                                                          RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a rat histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a spleen cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAMS0564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular disorders, non-insulin dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
                                             MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN
                              PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG
                                                                                                                                                                                                                                                                                                                                                                                   antiasthmatic; antiallergenic;
circulatory; antidiabetic; laxative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.2%; Score 1745; DB 5; Length 391;
84.9%; Pred. No. 9.6e-172;
ive 17; Mismatches 42; Indels
                                                                                                                                                  PLCHRRFQKAFWKILCVTKWPALSQNQSVSS 391
                                                                                                                                                                               PLCHRRFQKAFWKILCVTKQPALSQNQSVSS 391
                                                                                                                                                                                                                                                           AAM50566 standard; protein; 391 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-2001; 2001WO-US005914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-2000; 2000US-0208260P.
                                                                                                                                                                                                                                                                                                                                                                              Histamine H4 receptor; rat;
antiinflammatory; cardiant;
diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                     Rat histamine H4 receptor.
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N-PSDB; AAI70982.
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Best Local Similarity 84.99 Matches 332; Conservative

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DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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identification; agonist; screening; therapeutic; pharmaceutical; mutant.
                               1 MSESNGTDVLPLTAQVPLAFLMSLLAFAITIGNAVVILAFVADRNLRHRSNYFFLNLAIS
                                                                                                                                                       DFFVGVISIPLYIPHTLENWNFGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAV
                                                                                                                                                                                                                                                                         121 SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT
MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391
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9905 - 0121852P
9905 - 0123944P
9905 - 0123944P
9905 - 0123946P
9905 - 0123948P
9905 - 0123948P
9905 - 0133949P
9905 - 013446P
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9905 - 013446P
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99US-0152524P.
99US-0156555P.
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20-NOV-1998
12-NOV-1999
12-NOV-1999
12-MAR-1999
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12-MAR-1999
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28-MAY-1999
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28-MAY-1999
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29-SEP-1999;
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Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening; transmembrane receptor; signal cascade.
                                                                             Human orphan G protein-coupled receptor hRUP7.
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                                     (first entry)
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                                                                                                                                                                                                                      WO200031258-A2
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                   13-OCT-1999;
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28-MAY-1999;
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28-MAY-1999;
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01-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1999
AAY71297;
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5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes transmembrane receptors, preferably human g protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 MILEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
                                                                                                                                                                                                                                                                                                                                                                                Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents.
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                                                                                                                                                                                                                                                              Dang HT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.9%; Score 1370.5; DB 3; Length 390; 68.1%; Pred. No. 6.5e-133; ive 40; Mismatches 82; Indels 3;
                                                                                                                                                                                                                                                              Chen R,
                                                                                                                                                                                                                                                              Behan DP, Lehmann-Bruinsma K, Chalmers DT, C
Gore M, Liaw CW, Lin I, Lowitz K, White C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 89-90; 187pp; English
                                                                           99US-0157281P.
99US-0157282P.
99US-0157293P.
99US-0157294P.
                  99US-0156634P.
99US-0156653P.
99US-0157280P.
                                                                                                                                                                                                                                                            Lehmann-Bruinsma K,
                                                                                                                                                            99US-00416760
                                                                                                                                                                               99US-00417044
99US-0156633P
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Best Local Similarity 68.19
Matches 267; Conservative
                                                                                                                                                                                                                      (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                                                                          WPI; 2000-317986/27.
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                  29-SEP-1999;
29-SEP-1999;
01-OCT-1999;
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01-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and the encoding cDNAs for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in healthy and pathological states
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human orphan G protein-coupled receptors use in the identification of G protein-coupled
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98US-0109213P.
                              99US-0120416P.
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Best Local Similarity 68.1
Matches 267; Conservative
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AAY71297 standard; protein; 390 AA.

RESULT 5
AAY71297
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Local Similarity 68.1%
hes 267; Conservative
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                                                                 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
                                                                                               SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180
                                                                                                                                                                                    241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG 300
                                                                                                                                                                                                                                RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
                                                                                                                                                                                                                                             G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic; antinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human; osteopathic; neuroprotective; nootropic; dermatological; gynecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            013, encoded by cDNA of NCIMB 41073. The PFI-013 protein can be expressed by standard recombinant methodology. Antibodies and modulators of PFI-013
                                                    DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVXNIVLISYDRYQSVSNAV 120
                                                                                                                                                                                                          SASTEVPASFHSERORRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHOREHVELLRA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New G-protein coupled receptor-like polypeptide, polynucleotide for screening drug candidates for treating diseases associated with signal transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-
          SFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL
                                                                                                           SYRIQHIGVLKIVILMVAVWVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT
                                                                                                                                         181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN
                                                                                                                                                                                                                                                                           PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
                                                                                                                                                                                                                                                                                        Human GPCR-like polypeptide, PFI-013.
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                                                                                                                                                                                                                                                                                                                                                       AAB62445 standard; protein; 390
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20-APR-2000; 2000GB-00009973.
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(PFIZ ) PFIZER INC.
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N-PSDB; AAF83203
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are useful in the manufacture of a medicament for treating allergic disorders, including extrinsic asthma, immunological disorders, such as intrinsic asthma, vasculitic granulomatous disease, interstitial and other pulmonary disease, including chronic obstructive pulmonary disease other pulmonary disease, such as inflammatory bowel disease and neoplastic and myeloproliferative diseases. They are also useful for treating obseity, diabetes, metabolic, neurological diseases, psychotherapeutics, urogenital disease, reproduction and sexual medicine, inflammation, cancer, tissue repair, dermatology, photoageing, skin pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases, allergy and respiratory disease, sensory organ disorders, sleep disorders and hair loss. The PFI-013 protein and nucleic acid are useful in the diagnosis and treatment of the above conditions and also for screening crung candidates for the treatment of diseases associated with signal transduction. The antibodies are also useful for enrichment of cosinophils from mammalian, especially human blood and for detecting the protein in biological samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
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68.1%; Pred. No. 6.5e-133;
ive 40; Mismatches 82; I
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10-MAY-2001.
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                                                                                                                       G protein-coupled receptor protein BG26, with activity of binding to histamine and capable of changing intracellular cAMP concentration in response to its stimulus, applicable as tool in screening ligands or drug
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                                                                                                                                                                                                                                                                                                                     66.9%; Score 1370.5; DB 4; Length 390; 68.1%; Pred. No. 6.5e-133; ive 40; Mismatches 82; Indels 3;
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                                                                  Ohta M;
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                                                                                                                                                                                   Claim 1; Page 41-44; 50pp; Japanese.
                                                                  Tanaka K,
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20-DEC-2000; 2000WO-JP009038
                      99JP-00361687
                                           (BANY ) BANYU PHARM CO LTD.
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                                                                  Itadani H, Nakamura T,
                                                                                        WPI; 2001-441675/47.
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                    N-PSDB; AAH47911
                                                                                                                                                                                                                                                                                                 Sequence 390 AA;
                      20-DEC-1999;
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bulimia; osteoporosis; asthma; allergy; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcer; migraine; vontting; myocardial infarction; stroke; ulcer; migraine; vontting; manic depression; bipolar disorder; depression; delizophrenia; manic depression; bipolar disorder; depression; delizium; dementia; severe mental retardation; dyskinesia; Parkinson's disease; Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte; macrophage; eosinophil; neutrophil; function modulation; autoimmune disorder; pulmonary disorder; gene therapy; vaccine; drug screening; signal transduction; transgenic animal; drug discovery.
protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
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Homo sapiens.

WO200133221-A1

26-OCT-2000; 2000WO-US029461

02-NOV-1999; 99US-00431898. 03-FEB-2000; 2000US-00497790.

(SMIK ) SMITHKLINB BEECHAM CORP. (SMIK ) SMITHKLINB BEECHAM PLC.

Li X; Graybill TL, Fitzgerald LR, zhu Y; Bergsma DJ, Fi D, Morrow DM, Michalovich D, Aubart KM,

WPI; 2001-316464/33 N-PSDB; AAH24007 Novel G-protein coupled receptor polypeptide and polynucleotide for treating cancer, autoimmune, pulmonary, cardiovascular and neurological disorders and for identifying modulators useful for treating asthma.

Claim 1; Page 50-51; 54pp; English.

the detection of mutations in the corresponding gene. AXOR35 proteins are also useful for inducing an immunological response in a mammal against also useful for inducing an immunological response in a mammal against the above diseases, and for antibody production. AXOR35 nucleotides are expression studies, and for producing transgenic animals useful in drug discovery. AXOR35-specific antibodies are useful for purifying the AXOR35 protein or fragments thereof, and are also useful for treating conditions sequence represents human AXOR35 protein. The present The invention relates to the human G protein-coupled receptor AXOR35 (AAB73621), to cDNA encoding AXOR35 (AAB74006), and to AXOR35 fragments and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative transmembrane domains and is involved in signal transduction. AXOR35 has homology and structural similarity with G protein-coupled receptors such as the human histamine H3 receptor. The invention also relates to expression vectors and host cells comprising AXOR35 DNA, to recombinant expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins and nucleotides may be used to treat a wide variety of disorders including bacterial, fungal, protozoal and viral infections, particularly HIV-1 or HIV-2 infections; pain, cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia, bulimia; osteoporosis; asthma; allergies; urinary retention; acute heart failure; hypertemical, ingina indian pertoris; myocardial infarction; stroke; ulcers; migraine; vomiting; pertoris; myocardial infarction; stroke; ulcers; migraine; vomiting; psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retardation, and dyskinesias, such as Parkinson's disease, Huntington's disease or Gilles de la Tourette's syndrome. AXOR35 proteins and nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and antibodies may be used in screening compounds for their ability to modulate AXOR35 activity or expression. Such AXOR35 modulators are particularly useful for treating asthma, and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils or neutrophils in asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also useful for diagnosing or determining susceptibility of an individual to a disease via the detection of abnormal levels of protein or mRNA, or via

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DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor; signal transduction; mental disorder; central nervous system disease; metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder; psychotic disorder; Huntington's disease; schizophrenia; migraine; depression; anxiety; bipolar disorder; dementia; Alzheimer's disease; barkinson's disease; proliferative disorder; cancer; psoriasis; benign prostatic hypertrophy; diabetes; dyslipidaemia; obesity; anorexia; thyroid disorder; cardiovascular disease; hypotension; hypertension; thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;
                                                                                                                                                                                                                                           1 MPDINSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVUDKNLRHRSSYFFLNLAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT
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                                                                                                                                       Gaps
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                                                                                                                                       3;
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                                                                   DB 4; Length 390;
                                                                                                                                    Indels
                                                                                                                                       82;
                                                                ; Score 1370.5; DB 4; Pred. No. 6.5e-133; 40; Mismatches 82;
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/label= Transmembrane_domain_2
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/label= Transmembrane_domain_3
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                                                            66.9%;
68.1%;
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                                                                                                Best Local Similarity
Sequence 390 AA;
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Invention also discloses the use of these disorders, datus in screening disorders, or for the diagnosis of these disorders. GPCR-2067 nucleic disorders, or for the diagnosis of these disorders. GPCR-2067 nucleic caids may additionally be used to generate transgenic animals, including knockout animals, which may provide an integht into treating a variety of human disorders, and may also be used in the design of antisense conditions to suppressing expression of nGPCR-2067 in cells. nGPCR-2067, and GPCR-2067 modulators may be used to treat a wide variety of medical conditions, particularly mental disorders, central nervous system. Conditions, particularly MIV-1 or HIV-2 infections; pain; central nervous system, neurological and psychotic disorders such as Huntington's disease, schizophrenia, migraine, depression, anxiety, bipolar disorder, disease, and Parkinson's disease; proliferative disorders such as disease, and Parkinson's disease; proliferative disorders such as diabetes, dyslipidaemia, obesity, and metabolic disorders such as diabetes, dyslipidaemia, obesity, and concexia; thyroid disorders; cardiovascular diseases such as hypotension, thrombosis, inflammatory conditions, autoimmune disorders (e.g., rheumatoid arthritis); hormonal disorders; and renal failure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a novel human G protein-coupled receptor (GPCR) designated nGPCR-2067. Like all GPCRs, nGPCR-2067 has 7 putative transmembrane domains and is involved in signal transduction. The invention also relates to expression vectors and host cells comprising nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-2067, to antibodies specific for nGPCR-2067, to drug screening methods that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067 nucleic acid sequences may be used to isolate nGPCR-2067 allelic variants and species homologues and may also be used in genetic mapping. The invention also discloses the use of nGPCR-2067 nucleic acids in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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                                                           305. .326
/label= Transmembrane_domain_6
                                                                                                    342. .360
/label= Transmembrane_domain_7
  Transmembrane_domain_4
                                         'label= Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                Wood LS;
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                                                                                                                                                                                                                                                                                                                                                                                Vogeli G,
                                                                                                                                                                                                                                                                                                                                      (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                     08-MAY-2001; 2001WO-US014750.
                                                                                                                                                                                                                                                                                               08-MAY-2000; 2000US-0203108P.
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Best Local Similarity 68.1%
Matches 267; Conservative
  label=
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human; histamine receptor; chromosome 18; anti-inflammatory; anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke; anti-migranine; cardiant; anti-rheumatic; anti-arthritic; antipsoriatic; neuroprotective; inflammation; asthma; allergy; atopic dermatitis; myocardial infarction; migraine; chron; obstructive pulmonary disease; rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;
                 SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180
                                                                                                           179 SFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL 238
                                                                                                                                                   241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG 300
                                                                                                                                                                                      239 SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA 298
                                                                                                                                                                                                                           301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the amino acid sequence of a human histamine receptor (HR) designated SP9144. The sequence was isolated by searching databases with the sequence of known G-coupled protein receptor (GCPR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoaffinity chromatography, in immunoassay of histamine receptor, to identify cDNA clones that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma,
                                                                          181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding antigenic part of human histamine receptor, useful for preparing antibodies, e.g. for treating-histamine related
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                                                                                                                                                                                                                                                                                                                         361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
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                                                                                                                                              1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
                                                                                                                                                                          1 MPDTNSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS
                                                                                                                                                                                                                                 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV
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            chronic obstructive pulmonary disease, rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis
                                                                                                                    Gaps
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allergy, atopic dermatitis, stroke, myocardial infarction, migraine
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                                                                                                                    82; Indels
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                                                                                   ; Score 1370.5; DB 5 ; Pred. No. 6.5e-133; 40; Mismatches 82;
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                                                                                      66.9%;
68.1%;
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                                                                                                                    267; Conservative
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HEDRICK J A.
LAZ T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MONSMA F J.
MORSE K L.
UMLAND S P.
                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hormone secretion.
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                                                          Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WANG S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-1999;
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                                                                                         Query Match
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(WANG/)
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                                                                               Novel mammalian histamine receptor polypeptide useful for identifying agonist or antagonist for treating diseases such as inflammation, asthma, stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a histamine receptor. The polypeptide is useful for identifying an agonist or antagonist of a mammalian histamine receptor. It is useful as an antigen to elicit the production of antibodies. The histamine receptor polypeptide and polymucleotide are useful in the treatment and management of diseases such as inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infection, migraine, chronic obstructive pulmonary disease (COPD), rheumation arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis. They are also useful for modulating intracellular second messenger pathway activated through histamine receptors (cyclic-AMP, calcium, inositol phosphate and mitogen activated protein (MAP) kinase), changes in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                  239 SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKWGSFSQSDSVALHQREHVELLRA
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            SP;
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            Umland
                                                                                                                                                                                                                                                                                                                                                       Length 390;
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                                                                                                                                                                                                                                                                                                                                                                              82; Indels
            Morse KL,
                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                                                                                                                                      66.9%; Score 1370.5; DB 5 68.1%; Pred. No. 6.5e-133;
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            Monsma FJ,
                                                                                                                                                                                                                                                                                                                                                                            40; Mismatches
                                                                                                                                                                                                                                                                                                      mobilization, mitogenic effects, etc
                                                                                                                                Claim 2; Page 16-17; 21pp; English
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            Laz TM,
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hes 267; Conservative
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            Hedrick JA,
                                             2002-673827/72.
                                               WPI; 2002-673827
N-PSDB; ABW78739
                                                                                                                                                                                                                                                                                                                              Sequence 390 AA;
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            Behan JX,
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Best Local S
Matches 267
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New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 MILEFILIPVISVAYFWVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of a human histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a bone marrow cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor activity. Recombinant protein is useful for identifying modulators of the human histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSESNSTGILPPAAOVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
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cardiant; circulatory; antidiabetic; laxative;
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68.1%; Pred. No. 6.5e-133;
.ive 40; Mismatches 82; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-2000; 2000US-0208260P.
                                                                                                                                                                                                                                                                                                                                 22-FEB-2001; 2001WO-US005914
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                                      diagnosis; gene therapy
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Best Local Similarity
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                                                                                                              Homo sapiens
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9 9 us-10-626-445-8.rag

359 PLCHKRFOKAFLKIFCIKKOPLPSOHSRSVSS 390

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The invention provides an isolated histamine receptor, H4, which binds ligands comprising imidazole attached to amine by an alkyl chain. The H4 exceptor can be expressed by standard recombinant methodology. Cells expressing H4 receptor protein at a detectable level can suppress cyclic adenosine monophosphate (cAMP) formation when contacted with the H4 receptor and antibodies are used for identifying H4 receptor modulation of histamine H4 receptors is useful for treating transplanted organ rejection, asthma, allergies and autoimmune pathologies such as multiple sclerosis, type I diabetes, rheumatoid arthritis, cognitive and memory defects. The H4 receptor protein and nucleic acids are useful targets to identify drugs that are effective in treating disorders associated with histamine-regulated processes. Identification and isolation of H4 receptor provides for development of screening of molecules that interact with H4 receptors.
                                                                                                                                            Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive; antiasthmatic; antiallergic; neuroprotective; antidiabetic; human; cerebroprotective; cAMP modulator; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New histamine receptor, termed H4 useful for detecting H4 (ant)agonists for treating transplanted organ rejection, asthma, allergy, multiple sclerosis and rheumatoid arthritis.
                                                                                                                                                                                                                                                               "transmembrane domain"
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                                                                                                                  Human histamine H4 receptor protein.
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                            AAG66023 standard; protein; 390
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2000US-0227567P.
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172. .19
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130. .1
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304..3
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342. .3
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                                                                                                                                                                                                          Homo sapiens
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Genetic variants of H4 can be used to diagnose an H4 associated disease as described above. The H4 receptor polymuclectide is useful to treat or prevent a disorder associated with the function of H4 in peripheral blood leukcoytes. The present sequence represents the human histamine H4
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New G-protein coupled receptor polypeptides, useful for identifying modulators of signal transduction for treating kidney disease, hyperlipidemia, obesity, dyslexia and cardiac myxoma.

Claim 26; Page 61; 78pp; English

The present invention relates to a new G-protein coupled receptor (GPCR) polypeptide comprising greater than 70% amino acid sequence identity to the amino acid sequence of human GPCRS TGR62, TGR130.1, TGR130.2, human TGR213 or TGR22, 80% amino acid sequence identity to mouse TGR18 or 90% amino acid sequence identity to human novel edg receptor protein, as defined in the specification. The GPCR covalently linked to a solid phase is useful for identifying a compound that modulates signal transduction. The identified compounds are useful for treating kidney disease, cerebral covarenous malformations, hyperlipidenia, obesity, dysbaxia and cardiac myxoma. The molecules of the invention are useful for diagnosing disorders or conditions such as kidney-related conditions or diseases or such as renal failure, nephralitis, nephrolic syndrome, asymptomatic urinary abnormalities, renal tubule defects, hypertension and cardiac nephrolithiasis, liver-related disease or condition e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice and spleen-associated disorders and others. Modulation of the polypeptide of the invention is useful to treat or prevent any of the above conditions or diseases. The present amino acid sequence represents the human GPCR TGRE2 protein of the invention. Table invention. Table invention. Table invention and sequence represents the human GPCR TGRE2 protein of the invention. This sequence is one of seven novel G

Sequence 390 AA;

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Human; receptor; G-protein coupled receptor; AXOR35; lymphocyte; macrophage; ecsinophil; neutrophil; infection; transplant rejection; gastrointestinal disorder; gastrio ulcer; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; vonfliammatory bowel disease; atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis; psoriasis; urological disease; unimary retention; cardiovascular disease; myocardial infarction; hypotransion; hypertension; pulmonary disorder; chronic obstructive pulmonary disease; cough; renal disease; rechamical arterioscalerosis; atheroscalerosis; psychosis; psychosis; disorder; migraine; anorexis; anorexis; anorexis; anorexis; dyskinesia; Parkingon's disease; cancer; obesity; stroke; septic shock;
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Homo sapiens.

JS2002137054-A1

26-SEP-2002.

20-JUL-2001; 2001US-00910411.

99US-00431898 2000US-00497790 02-NOV-1999;

20-OCT-2000; 2000US-00693761.

(SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.

Ŀ Į, Graybill Fitzgerald L, zhu Y; Morrow DM, Aubart KM, Bergsma DJ, Michalovich D, Morrow D 

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WPI; 2003-074982/07. N-PSDB; ABS57063.

Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infections, gastrointestinal disorders, autoimmune disorders, urological diseases, cardiovascular diseases and cancer.

Claim 1; Page 22; 24pp; English.

The invention relates to an isolated G-protein coupled receptor

C polypeptide, AXOR35, (and its homologues and variants) and its encoding

C polypucideotide (and its homologues, variants, complements and RNA

cquivalents). Also included are an anti-AXOR35 antibody, an AXOR35

cquivalents). Also included are an anti-AXOR35 antibody, an AXOR35.

C expression vector, producing a recombinant host cell by introducing the

c expression vector, producing a recombinant host cell by introducing the

c expression vector, and inhibiting or promoting the function of

the host cell expressing AXOR35, identifying/screening for agonists or

antagonists of AXOR35 and inhibiting or promoting the function of

C lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,

by administering to the patient AXOR35 agonists or antagonists. The

agonist or antagonist identified is useful for treating a disease such as

asthma, or for inhibiting or promoting the function of lymphocytes,

c asthma, or for inhibiting or promoting the function of lymphocytes,

c antagonist or sosinophils, or neutrophils in diseased tissue such as an

asthmatic lung. AXOR35 or polymucleotide is useful in diagnostic assays,

for identifying compounds that are agonists or antagonists of AXOR35, as

vaccines, or for transplant rejection, gastrointeetinal disorders (

c viral infections), transplant rejection, gastrointeetinal disorders (

c riritable bowel syndrome, vonditing, inflammation (such as tropic

dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,

c arteriosclerosis, atherosclerosis, psychotic and neurological disorders

(such as migraine, anorexia, anxiety, schizophrenia), dypkinesias (such

c arteriosclerosis, atherosclerosis, psychotic and neurological disorders

(such as maigraine, anorexia, anxiety, schizophrenia), dypkinesias (

such as parkinson's disease, cancer, obesity, settoke, septic sphock, gareft

c cough, reans and osteoporosis. The present sequence represents human AXOR35

Sequence 390 AA;

Human G-protein coupled receptor AXOR35.

28-JAN-2003 (first entry)

ABG71960;

8×4×4×8

ABG71960 standard; protein; 390 AA

RESULT 15 ABG71960

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A Molecule type: mRNA
A; Residues: 1-460 < KUB>
A; Residues: 1-460 < KUB>
A; Residues: 1-460 < KUB>
A; Cross-references: UNIPROT: P04761; UNIPARC: UPI00001252AD; GB: X04413; NID: g1863; PIDN: C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosp F; 25-50 Domain: transmembrane #status predicted < TMI>
F; 25-50 Domain: transmembrane #status predicted < TM3>
F; 100-121 Domain: transmembrane #status predicted < TM3>
F; 142-168 Domain: transmembrane #status predicted < TM5>
F; 187-209 Domain: transmembrane #status predicted < TM5>
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A24325
R;Kubo, T.; Fukuda, K.; Mikami, A.; Maeda, A.; Takahashi, H.; Mishina, M.; Haga, Nature 323, 411-416, 1986
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355 FSLVKEKKAARTLSAILLAFILTWTPYNIMVLV-STFCKDCVPETLW-ELGYWLCYVNST 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Cloning, sequencing and expression of complementary DNA encoding the A;Reference number: A24325; MUID:87014801; PMID:3762692 A;Accession: A24325
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C;Species: Rattus norvegicus (Norway rat)
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A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-460 < CHA>
A; Cross-references: UNIPROT: P11229; UNIPARC: UPI00001252AB; EMBL: X52068; NID: 934450; PIDN
A; Once: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
B; Allard; W.J.; Sigal, I.S.; Dixon, R.A.F.
Nucleic Acids Res. 15, 10604, 1987
A; Raterence of the gene encoding the human MI muscarinic acetylcholine receptor.
A; Reference number: $06327; MUID: 88096607; PMID: 3697105
A; Recession: $06327
A; Molecule type: DNA
A; Residues: 1-460 < ALL.
A; Accession: Social Ail A; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J
EMBO J. 6, 3928-3929, 1987
A; Cross-references: UNIPARC: UPI00001252AB; Smith, D.H.; Ramachandran, J.; Capon, D.J
EMBO J. 6, 3928-3929, 1987
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A;Residues: 1-172,'M',174-460 <PER>
A;Cross-references: UNIPARC:UPI00005040F; EMBL:X15263; NID:g32317; PIDN:CAA33334.1; PID
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A;Reference number: $04326; MUID:88166632; PMID:3443095
A;Accession: $04326
                                                                                                                                                           muscarinic acetylcholine receptor M1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: 809508; S06327; $504326
R;Chapman, C.G.; Browne, M.J.
Nucleic Acids Res. 18, 2191, 1990
A;Title: Isolation of the human m1 (Hm1) muscarinic acetylcholine receptor gene by PCR
A;Reference number: 809508; MUID:90245684; PMID:2336407
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187-209/Domain: transmembrane #status predicted <TM5>
367-387/Domain: transmembrane #status predicted <TM6>
402-420/Domain: transmembrane #status predicted <TM7>
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84; Mismatches 150;
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Matches 122;
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Jul-2004	OY 306 SLAILLSAFALCWAPYCLFTIVLSTYPRTERPKSVMYSIAFWLQWFNSFVNPFLYPLCHR 365
A; Reference number: JT0530; MUID:90166521; PMID:3272174 A; Reference number: JT0530; MUID:90166521; PMID:3272174 A; Accession: JT0531 A; Molecule type: DMA A; Deciding an accession of the period of	RECKARMATICATEM  :     :  ::  TFRKTF-KLLLCRW
A.Cross-references: UNIPROT:P08911; UNIPARC:UPI00001252BF R;Liao, C.F.; Themmen, A.P.N.; Joho, R.; Barberis, C.; Birnbaumer, M.; Birnbaumer, L. J. Biol. Chem. 264, 7128-7337, 1989 A;Title: Molecular cloning and expression of a fifth muscarinic acetylcholine receptor. A;Reference number: A33354; MUID:89214170; PMID:2540186	RESULT 5 S01114 muscarinic acetylcholine receptor M2, glandular - pig N,Alternate names: muscarinic acetylcholine receptor III C.Species: Sus scrofa domestica (domestic pig)
A;Accession: A33354 A;Molecule type: DNA A;Residues: 1-531 <lia></lia>	C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004 C;Accession: S01114 R:Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.
A;Cross-references: UNIPARC:UP100001252BF; GB:M22925; NID:g205311; PIDN:AAA41572.1; PID: A;Note: the nucleotide sequence for residues 101-120 and the translation 121-140 are not A;Note: the authors translated the codon CAG for residue 19 as Glu, AAC for residue 65 a R:Kurtenbach, B.: Curtis, C.A.M.: Pedder, B.K.: Aitken, A.: Harris, A.C.M.: Hulme, B.C.	FEBS Lett. 235, 257-261, 1988 A;Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonis A;Accesion: number: S01114; MUID:88296835; PMID:3402600 A;Accession: S01114
J. Biol. Chem. 265, 13702-13708, 1990 A;Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invo A;Reference number: A37121; MUID:90337982; PMID:2380182	A;Molecule type: DNA A;Residues: 1-590 <aki> A;Residues: 1-590 <aki> C;Cross=references: UNIPROT:P11483; UNIPARC:UPI00001252B7; EMBL:X12712; NID:g1861; PIDN:C</aki></aki>
A;Status: preliminary A;Molecule type: protein A;Residues: 66-128 **KIR*	Cycopyclaum; Tycocin-Coupled receptor; glycopycotein; neurotransmitter receptor; transmen F;68-91/Domain: transmembrane #status predicted <tm1> F;108-21/Domain: transmembrane #status predicted <tm2> F;108-105/Angeria Fire Fire Fire Fire Fire Fire Fire Fire</tm2></tm1>
A/CLOBBS-ILLERINGES: UNITARY.OFF.0001/1002 C/COmment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotr C/Superfamily: vertebrate rhodopsin C/Reywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho F/29-52/Domain: transmembrane #status predicted	F/132-207/Domain: transmembrane #status predicted <tm4> F/231-252/Domain: transmembrane #status predicted <tm5> F/231-252/Domain: transmembrane #status predicted <tm5> F/528-513/Domain: transmembrane #status predicted <tm6> F/528-546/Domain: transmembrane #status predicted <tm70></tm70></tm6></tm5></tm5></tm4>
atus predicted <t status predicted status predicted status predicted</t 	Query Match 20.0%; Score 410.5; DB 2; Length 590; Best Local Similarity 24.8%; Pred. No. 8e-28; Matches 125; Conservative 82; Mismatches 136; Indels 161; Gaps 16;
status status (Asn)	Qy 18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL 77  1
<pre>'Query Match 'Query Match Best Local Similarity 24.6%; Pred. No. 7.1e-28; Matches 122; Conservative 92; Mismatches 140; Indels 141; Gaps 15;</pre>	
. 16 VPLAFLMSSFAFAIMVGNAVVILAFVVDRNIRHRSNYFFLNLAISDFLVGLISIPLYIPH 75 : :   : : : :     : : :     :   :   :	133 VAQNVAVWILAFLVNGPMILASDSWKNSTNTKOCEPGFVTEWYLLTITMLLEFILL
Qy 76 VLF-NWNFGSGICMFWLJTDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIM 130	4 2
Qy 131 KIVAQMVAVWILAFLVNGFMILASDSWKNSTNTKDCEPGFVTEWYLLTITMLLEF 185	246 SAASR
Qy 186 LLPVISVAYFNVQIYMSLWKR	298 QSLKRSAKKKYGKCHFWFTTKSWKFSAEQMUQUHSSSUSWNNNUAAASLEENSASSUEEDI 255PRRKSSILVSLRTHMNSITAPKV
OY 214SHAGPSTTSSSASGHLHRAGVACRTSNPGLKESA 247  DD 262 QRERNQASWSSSRRSTSTTGKTTQATDLSADWEKAEQVTTCSSYPSSEDEAKPTTDPVFQ 321	358 GSETRALYSIVLKLPGHSTILNSIKLPSSDNLQVPEEELGIVDLERKASKLQAQKSMUDG 279 GSFWRSESAA
Qy 248ASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALR 290  322 MVYKSEAKESPGKESNTQETKETVVNTRTENSDYDTPKYFLSPAAAHRLKSQKCVAYKFR 381	418 GSFQKSFSKLPIQLESAVDTAKASDVNSSVGKTTATLPLSFKEATLAKKFALKIRSQLIR 292 REYAELLRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWF  :    ::    ::                 ::    : :    : :     ::     :
Qy 291	Db 478 RKRWSLIKEKKAAQTLSAILLAFIITWTPYNIMVLV-NTFCDSCIPKTYW-NLGYWLCY1 535 Qy 352 NSFVNPFLYPLCHRRFQKAFWKIL 375

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Matches 122; Conservative
                                                                                                                                                                                                                                     A, Status: preliminary
A, Molecule type: protein
A, Residues: 62-124 < KUR>
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A; Accession: A94293
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                                                                                                                         Rical, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roeske Adv. Exp. Med. Biol. 287, 313-330, 1991
A;Title: The molecular properties of the M1 muscarinic receptor and its regulation of cy A;Reference number: 151837; MUID:92101806; PMID:1759615
A;Accession: 151837
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UP10000046CE7; GB:S73971; NID:g241253; PIDN:AAB20705.1; PID:
Genetics:
A;Genetics:
C;Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLVGLISIPLYIPHVLF-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SYRAQHTGIMKIVAQMVAV-WILAFLVNGPMILASDSWKNSTNTK-----DCEPGFVTEW 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 YILTITMLLEFLLPVISVAYFNVQIYWSLWKR-----RAL----SRCPSHAGFSTTSSS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AS----SHLHRAGVACRT-----SNPGLKESAASRHSESPRRK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 RSQPGAEGSPESPPGRCCR---CCRAPRLLQAYSWKEEEEEDBGSMESLTSSEGEEP--G 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 SEVVIKMPMVDSEAQAPTKQPPKSSPNTVKRPTKKG---RDRGGKGQKPRGKEQLAKRKT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 AELLRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSF 354
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A94518; A94293; A37121; A29514
                                                                                     C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C;Accession: IS1837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                20.0%; Score 410; DB 2; Length 460; 27.4%; Pred. No. 6.7e-28; ive 83; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT:P08482; UNIPARC:UP10000046CE7
R,Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 VNPFLYPLCHRRFQKAFWKILCVTKW 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 27.4%;
Matches 122; Conservative 6
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submitted to GenBank, July 1987
A;Reference number: A94518
A;Accession: A94518
                                                                   C;Species: Rattus sp. (rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 SSILVSL----
                                               muscarinic receptor - rat
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Best Local Similarity
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A; Residues: 1-460 <BO1>
                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-460 <RES>
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A,Molecule type: mRNA
A,Residues: 1-227,338-460 <BO2>
A,Residues: 1-227,338-460 <BO2>
A,Cross-references: UNIPARC:UPI00001778CE; UNIPARC:UPI00001778CF
A,Experimental source: cerebral cortex
A,Note: only a part of the protein translation is given; none of the nucleotide sequen
B,Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C
J. Biol. Chem. 265, 13702-13708, 1990
A,Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues in
A,Reference number: A37121; MUID:90337982; PMID:2380182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UP100001778D0
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosp. F;25-50/Domain: transmembrane #status predicted <TMl>
F;62-93/Domain: transmembrane #status predicted <TMl>
F;100-121/Domain: transmembrane #status predicted <TMl>
F;142-168/Domain: transmembrane #status predicted <TMl>
A;Title: Identification of a family of muscarinic acetylcholine receptor genes.
A;Reference number: A94293; MUID:87263421; PMID:3037705
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                                                                                                         C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: 84757.
E;Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.
Biochim. Biophys. Acta 1223, 151-154, 1994
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F;367-387/Domain: transmembrane #status predicted <TM6>
F;402-420/Domain: transmembrane #status predicted <TM7>
F;2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F,492-512/Domain: transmembrane #status predicted F;527-545/Domain: transmembrane #status predicted
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Matches 121; Conservative
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                                                                                                         Query Match
Best Local 3
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A;Residues: 1-589 <BRA>
A;Cross-references: UNIPROT:P08483; UNIPARC:UP10000170853; GB:M18088; NID:g202657; PIDN
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                                                                                                                                       A;Molecule rype: mRNA
A;Residues: 1-590 <LEE>
A;Cross-references: UNIPROT:P41984; UNIPARC:UP100001252B3; EMBL:U08286; NID:g520465;
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine; Reference number: S47572; MUID:94339178; PMID:8061048; Accession: S47572
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R;Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.
Biochem, Biophya. Res. Commun. 149, 125-132, 1987

A;Title: A novel subtype of muscarinic receptor identified by homology screening. A;Reference number: A29476; MUID:88077068; PMID:3120722
                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 MNRWALGNLACDLWLSIDYVASNASVMNLLVISFDRYFSITRPLTYRAKRTTKRAGVMIG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| | | :::|:: | | | | ::| | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG----FVTEWYILTITMLLEFLL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVISVAYFNVQIYWSLWKRRALSRCPSHAGF--STTSSSASGHLHRAGVACRTSNPGLKE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 PVTIMTI----LYWRIYKETE-KRTKELAGLQASGTEAEAENFVHPTGSSRSCSSYELQQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LRQ 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 OSMKRSARRKYGRCHFWFTTKSWKPSAEQMDQDHSSSDSWNNNDAAASLENSASSDEEDI 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL 77
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSETRAIYSIVLKLPGHSTILNSTKLPSSDNLQVPEEELGSVGLERKPSKLQTQQSMDDG
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Best Local Similarity 25.0%; Pred. No. 9.8e-28;
Matches 126; Conservative 83; Mismatches 134; Indels 161; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---PRRKSSILVSLRTH---MNS----SITAFKV-----
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                                                                                                                 Status: preliminary
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C;Accession: S10128
R;Peralta, B.G; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-1987, 1987.
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expre
A;Reference number: S04326; MUID:88166632; PMID:3443095
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P;105-131/Domain: transmembrane #status predicted <TM2>
F;143-164/Domain: transmembrane #status predicted <TM2>
F;143-164/Domain: transmembrane #status predicted <TM3>
F;131-252/Domain: transmembrane #status predicted <TM4>
F;231-252/Domain: transmembrane #status predicted <TM5>
F;493-513/Domain: transmembrane #status predicted <TM5>
F;493-513/Domain: transmembrane #status predicted <TM6>
F;525-546/Domain: transmembrane #status predicted <TM6>
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A;Cross-references: UNIPROT:P20309; UNIPARC:UPI0000050453; EMBL:X15266; NID:g32323; PIDN:
C;Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                                        NAVSYRAQHT----GIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG---- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 LGTVDVERNAHKLQAQKSMGDGDNCQKDFTKLPIQLESAVDTGKTSDTNSSADKTTATLP 454
                                                                                                                                                         28
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                      51 SNDISSDPLGGHIIWQVVFIAFLIGFLATIGNIIVIVAFKVNKQLKTVNNYFLLSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 SWINNDAAASLENSASSDEEDIGSETRAIYSIVLKLPGHSSILNSTKLPSSDNLQVSNED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : :|: :| |: :| || || || : :| : :| 455 LSFKEATLAKRFALKTRSQITKRKRMSLIKEKKAAQTLSAILLAFIITWTPYNIMVLV-N
                                                                                                                                                                                                                                                                                                           ISDFLVGLISIPLYIPHVLFN-WNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - FVTEWYILTITMLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGF - - STTSSSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 NFVHPTGSSRSCSSYELQQQGVXR---SSRRKYGRCHFWFTTKSWKPSAEQMDQDHSSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TAPKVGSFWRSESAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 GHLHRAGVACRTSNPGLKESAASRHSESPRRK-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SSILVSLRTHMNSSI-----
                                                                            Gaps
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tch al Similarity 23.8%; Pred. No. 3.6e-27; 25. Conservative 84; Mismatches 145; Indels 172;
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F;142-163/Domain: transmembrane #status predicted
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Matches 124; Conservative
                                                                                                                                                                                                            Matches 125; Conservative
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Best Local Similarity
                                                                                                                                                                                      Similarity
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A;Status: preliminary
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                                                                                                                                                                Query Match
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A;Cross-references: UNIPARC:UPI00001778C2
A;Cross-references: UNIPARC:UPI00001778C2
A;Cross-references: UNIPARC:UPI00001778C1; UNIPARC:UPI00001778C2
A;Cross-references: UNIPARC:UPI00001778C2
A;Cross-references: UNIPARC:UPI00001778C2
A;Cross-reference of the protein translation is given; none of the nucleotide sequence
B;Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
A; Maccardince acetylcholine receptors. Peptide sequencing identifies residues involation number: A37121; MUID:90337982; PMID:2380182
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Kyeywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F;67-90/Domain: transmembrane #status predicted <TMl>
F;104-124/Domain: transmembrane #status predicted <TM2>
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                          252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 FN-WNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHT----GIMKI 132
                                                                                                                                                                                      133 VAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG----FVTEWYILTITMLLEFLL 187
                                                                                                                                                                                                                                 191 LA-----WVISFVLWAPAIL---FWQYFVGKRTVPPGECFIQFLSEPTITFGTAIAAFYM 242
                                                                                                                                                                                                                                                                                                                            243 PVTIMTI----LYWRIYKETEKRTKELAGLQASGTEAETENFVHPTGSSRSCSSYELQQQ 298
                                                                                                                                                                                                                                                                                                                                                                               206 ----RRALSRCPSHAGFSTT-----SSSASGHLHRAGVACRTSNPGLKES 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 IGSETRAIYSIVLKLPGHSTILNSTKLPSSDNLQVPEEELGMVDLERKADKLQAQKSVDD 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 GGSFPKSFSKLPIQLESAVDTAKTSDVNSSVGKSTATLPLSPKEATLAKRFALKTRSQIT 476
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  LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         muscarinic acetylcholine receptor M3 - rat
C,Species: Rattus norvegicus (Norway rat)
C,Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C,Accession: B94518; B94293; B37121; B29514
                                                                                                                                                                                                                                                                                                                                                                                                         299 SMKRSNRRKYGRC--HFWFTTKSWKPSSEQMDQDHSSSDSWNNNDAAASLENSASSDEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --ESPRRKSSILVSLR-----THMNSSI-----TAFKVGS----FWRSESAALR
                                                                                                                                                                                                                                                                                    188 PVISVAYFNVQIYWSLWK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT: P08483; UNIPARC: UPI0000163B75 R;Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R. Science 237, 527-532, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 AASR-------HS------
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submitted to GenBank, July 1987
A;Reference number: A94518
A;Accession: B9518
A;Molecule type: mRNA
A;Residues: 1-589 <BOl>
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muscarinic acetylcholine receptor, M3 isoform - chicken

C;Species: Gallus gallus (chicken)

C;Species: Gallus gallus (chicken)

C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004

C;Accession: A55019

R;Gadbut, A.P.; Galper, J.B.
J. Biol. Chem. 269, 25823-25829, 1994

A;Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium ar A;Reference number: A55019; MUID:95014393; PMID:7929287
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C,Superfamily: vertebrate rhodopsin
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ISDFLVGLISIPLYIPHVLFN-WNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 NAVSYRAQHT----GIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPG---- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 QFLSEPTITFGTAIAAFYMPVTIMTI----LYWRIYKETE-KRTKELAGLQASGTEAEAE 277
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       F;184-206/Domain: transmembrane #status predicted <TM4>
F;230-251/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM6>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SNSTGILPPAAQ-----VPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLA 58
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|| : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : |
                                                                                                                                                                                                                                                                                                                                                                                                                                              19.6%; Score 402; DB 2; Length 589; 23.8%; Pred. No. 4.4e-27;
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Db   72 LIIGTFSMALYTTYLLMGHWALGTLACDLWLALDYVASNASVMALLLISFDRYFSVTRPL 131   SYRAGHTGIMKIVAGWIVAVARIAPLINGPMILASDSWKNSTNTKDCEPGFVTEW 174	muscarinic acetylcholine receptor M5 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000 C;Accession: JT0530 R;Donner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J. Neuron 1, 403-410, 1988 A;Vitle: Cloning and expression of the human and rat m5 muscarinic acetylcholine recepton A;Reference number: JT0530; MUD:90166521; PMID:3272174 A;Reference number: DNSA A;Molecule type: DNA	A; Residues: 1-532 <bon> A; Coss-references: UNIPARC: UP100001778C4 A; Cross-references: UNIPARC: UP100001778C4 C; Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotrs C; Superfamily: Vertebrate rhodopsin C; Superfamily: Vertebrate rhodopsin C; Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphog F; 30-53 Domain: transmembrane #status predicted <tm2> F; 50-53 Domain: transmembrane #status predicted <tm2> F; 105-126 Domain: transmembrane #status predicted <tm5> F; 147-169 Domain: transmembrane #status predicted <tm5> F; 444-464 Domain: transmembrane #status predicted <tm5> F; 444-464 Domain: transmembrane #status predicted <tm5> F; 419-498 Domain: transmembrane #status predicted <tm7> F; 813/Binding site: carbohydrate (Asn) (covalent) #status predicted</tm7></tm5></tm5></tm5></tm5></tm2></tm2></bon>	Query Match Best Local Similarity 24.6%; Pred: No. 6.5e-27; Matches 122; Conservative 90; Mismatches 142; Indels 141; Gaps 15;  Qy
Oy 16 VLF-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDBYQSVSNAVSYRAQHTGIM 130   :	LOWFNSFVNPFLYPLCHRRFQKAFWKIL 375    :                     :   :   :	nerer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M. 18397-18403, 1988 sequence, and instinal expression of the mouse M1 muscari. A92694; MUID:89054021; PMID:2848036 A92694; MUID:89054021; PMID:2848036 A92742 UNIPARC:UPI00001778CD Translated the codon ATC for residue 119 as Thr herer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M. 6596, 1989	notation; erratum, correct translation of residue 119  notation; erratum, correct translation of residue 119  protein-coupled receptor; glycoprotein; neurotransmitter receptor in transmembrane #status predicted <tm3>  in: transmembrane #status predicted <tm3>  in: transmembrane #status predicted <tm3>  in: transmembrane #status predicted <tm5>  in: transmembrane #sta</tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm5></tm3></tm3></tm3>

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Job time : 26 secs
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R;Yasuoka, A.; Abe, K.; Arai, S.; Emori, Y.
Bur. J. Boicchen. 235, 501-507, 1996
A;Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Me
A;Reference number: S71323; MUID:96184522; PMID:8654394
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                                                                                           245 ESAASRHSESPRRKSSILVSLRTHMNSSI--TAFKVGSFWRSESAALR------ 290
                                                                                                                     323 VVYKSQGKESPGEEFSAEETEETFVKAETEKSDYDTPNYLLSPAAAHRPKSQKCVAYKFR 382
                                                                                                                                                                                      -- OREYAELLRGRKLAR 305
                                                                                                                                                                                                                   : | : | | |: 383 LVVKADGNQETNNGCHKVKIMPCPFPVAKEPSTKGLNPNPSHQMTKRKRVVLVKKRKAAQ 442
                                                                                                                                                                                                                                                                          306 SLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHR 365
                                                                                                                                                                                                                                                                                                  60 SDFLVGLISIPL-YIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 AVSYRAQHTGIMKIVAQMVAVWILAFLVN-GPMILASDSWKNSTNTKD--C---EPGFV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 TEWYILTIIMLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 --VVAQKESRGLKEGQKIEKSDSEQ-----VILRMHRGNTTV-----SEDEALRS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 REYAEL----LRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAF 346
  214 ----SHAGFSTT--SSSASGHLHRAG------VACRT-----SNPGLK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SNSTGILPP----AAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-1A adrenergic receptor - Japanese medaka
C;Species: Oryzias latipes (Japanese medaka)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 19.2%; Score 392.5; DB 2; Length 477; Best Local Similarity 28.0%; Pred. No. 2.3e-26; Matches 115; Conservative 65; Mismatches 145; Indels 85; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 WLOWFNSFVNPFLYPLCHRRFQKAFWKIL---CVTKWPA----LSQNQS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: S71323
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-477 < YAS>
A, CCOSS-references: UNIPARC:UPI00001778AD; EMBL:D63859
A, Note: it is uncertain whether Met-1 or Met-8 is the initiator C, Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 ----IFSAVGSFYLPLAIILAMYCRVY-------
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501 TFRKTF-KMLLLCRW 514
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Mus musculus (Mouse).
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Copyright (c) 1993 - 2006
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Maximum DB seq
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Perfect score:
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Ensembl; ENSMUSG0000037346; Mus musculus.

Mai, MG1: 4228635; HrA4.

GO; 00055615; C:extracellular space; RCA.

GO; GO:0005887; C:integral to plasma membrane; IC.

GO; GO:0005887; C:membrane fraction; IDA.

GO; GO:0001884; F:histamie receptor activity; IDA.

GO; GO:0001884; F:histamie receptor activity; IDA.

GO; GO:0001886; P:inflammatory response; TAS.

InterPro; IPR000276; GPCR_Rhodps
InterPro; IPR008102; Histami H4 ropt.

PANTHER; PTRR19266:SF82; Histamirecept_H4; 1.
                                      macaca mula
                                                                         brachydanio
                                                                                         cavia porce
macaca mula
                                                                                                                                                                                     homo sapien
                                                                                                                                                                                                       pongo pygma
lepomis mac
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P08911 rattus norv
                                                    caenorhabdi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C., Wilson S., Kuei C., Lovenberg T.W.;
Submitted (MAR-2001) to the EMBL/GenBank/DBbJ databases.
-!- SUBCELLULA LOCATION: Membrane (By similarity).
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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0
                     Q48ac4
P56489
                                                    Q61w39
Q5u3d9
                                                                                         Q8vh24
P56490
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P11229
P04761
                                                                                                                                                                                    Q53xz3
Q5r949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOPSN.

PRINTS; PR01756; HISTAMINEH4R.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

G-protein coupled receptor; Membrane; Receptor; Transducer; Transembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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Pred. No. 2e-138;
                                                                                                                                                                                                                                                                                                                                                                                                            091272;
01-DEC-2001, integrated into UniProtKB/TrEMBL.
01-DEC-2001, sequence version 1.
21-FEB-2006, entry version 23.
Histamine H4 receptor.
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                             QASANA ACMI MACMU

QG1W39 CAEBR

QG1W39 CAEBR

QG0W124 CAVVO

ACMS MACMU

QG6W11 HUMAN

ACM1 HUMAN

ACM1 PIG

QS5R949 PONDYY

Q4PLW4 LEPPMA
                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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Q8N149 HUMAN
Q4SAC4_TETNG
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390; Conservative
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                  61 DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
                                                          SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180
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                                                                                                                         MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240
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                                                                                                                                            181 MLLEFLLPVISVAYFNVOIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN
                                                                                RKLARSLAIILSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 85.2%; Score 1745; DB 2; Length 391; Local Similarity 84.9%; Pred. No. 1.5e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Membrane; Receptor; Transducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 AA; 44023 MW; C707BA6E39CFED41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGD; 620631; Hrh4.
GO; GO:0004969; F:histamine receptor activity; IDA.
GO; GO:0006964; F:histamine receptor activity; IDA.
GO; GO:0006964; F:inflammatory response; IMP.
InterPro; IPR000276; GPCR Rhodgen.
InterPro; IPR00127; Histamn. H4_ropt.
PANTHER: PTHR19266:SF82; Histamnrecept_H4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF358860; AAK97381.1; -; mRNA.
Ensembl; ENSRNOG0000016887; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001, integrated into UniProtKB/TrEMBL.
01-DEC-2001, sequence version 1.
21-PEB-2006, entry version 22.
                                                                                                                                                                                                                                                                                                                  PLCHRRFQKAFWKILCVTKWPALSQNQSVSS 391
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
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Q91ZY1;
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Ensembl; ENSG0000134489; Homo sapiens.

Ensembl; ENSG0000134489; Homo sapiens.

GO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0016182; E:receptor activity; IEA.

GO; GO:001584; P:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:rocoptor outline receptor protein signalin. . .; IEA.

GO; GO:0007185; P:signal transduction; IEA.

InterPro; IPR000276; GFCR. Rhodopsin.

InterPro; IPR001027; Histamn H4 ropt.

PANTHER; PTHR19266:SF82; HistamnH4 ropt.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                 61 DFFVGVISIPLYIPHTLFNWNFGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAV
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Membrane; Receptor; Transducer; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               390 AA; 44470 MW; CC82B5D30D216C66 CRC64;
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01-DEC-2001, sequence version 1.
1-FBB-2006, entry version 20.
Histamine receptor H4.
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
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NUCLEOTIDE SEQUENCE
TISSUE=PCR rescued
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                                                              NIH MGC Project;
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ralausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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"Mannan A. Schein J.E., Jones S.J.M., Marra M.A.;

"Mannan A. Schein J.E., Jones S.J.M., Marra M.A.;

"Mannan A. M. Mannan A. Mannan A. Marra M.A.;

"Mannan A. Mannan A. Mannan A. Marra M.A.;

"Mannan A. Mannan A. Mannan A. Marra M.A.;

"Mannan A. Mannan A. Man
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                       Gaps
                                                                                       3;
                               Length 390;
                                                                                    81; Indels
                               DB 2;
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                            67.0%; Score 1372.5; DB 68.1%; Pred. No. 1.1e-90; ive 41; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2006, integrated into UniProtKB/TrEMBL
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                                                           Best Local Similarity 68.19
Matches 267; Conservative
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Q2M2N7;
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                                  Query Match
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Q2M2N7_MOUSE
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                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Q9H3RD; 9QGGQD,
01-UTIN-2001, integrated into UniProtKB/Swiss-Prot.
01-UTIN-2001, sequence version 2.
01-UTIN-2006, entry version 43.
Histamine H4 receptor (HH4R) (GFRV53) (G-protein coupled receptor 105) (GPCR105) (SP9144) (AXOR35).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 MKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTITMLLEFLLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 RHSESPRKKSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRGRKLARSLAI
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MEDILE-20238417, PubMed=10973974; DOI=10.1074/jbc.M006480200;

MODINE-20238417, Morikawa N., Saito Y., Masuho Y., Matsumoto S.;

"Molecular cloning and characterization of a novel type of histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.; "Molecular cloning and characterization of a new human histamine
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MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;
                                                                                                                                                                                                                                                                                                                                                 Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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                                                                  Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                       EMBL; BC111862; AAI11863.1; -; mRNA.
SEQUENCE 262 AA; 29860 MW; 1A0CAF2085E09779 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor preferentially expressed in leukocytes.";
J. Biol. Chem. 275:36781-36786 (2000).
                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                 Score 1372; DB 2;
Pred. No. 7.7e-91;
0; Mismatches 1;
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Jones P.G., Wu S., Betty M.;
"Cloning of a novel histamine receptor.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 AFWKILCVTKWPALSQNQSVSS 391
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                                                                                                                                                                                                                                                                                                                                                                                  99.68;
rescued clones;
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 261; Conservative
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us-10-626-445-8.rup

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BAB20091.1; -;
                                                                                                                                                     JC7566; JC7566.
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206 2
253 2
390 AA;
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                                                                                                                                                                                                                          606792; gene.
  AB045370;
                         AF307973;
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--- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.

--- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and cosinophils. Shows preferential distribution in cells of immunological relevance such as T-cells, dendritic cells, monocytes, mast cells, neutrophils. Also expressed in a wide variety of periphral tissues, including the heart, kidney, liver, lung, pancreas, skeletal muscle prostate, small intestine, spleen, fetal liver and lymph node.

--- INDUCTION: Expression is either up-regulated or down-regulated upon activation of the lymphoid tissues and this regulation may depend on the presence of IL-10 or IL-13.

--- MISCELLANEOUS: Does not bind diphenhydramine. Shows modest affinity for dimappit, impromidine, clobenpropit, thioperamide, burimamide clozapine, immepip and imetit. The order of inhibitory activity was imetit - sclobenpropit burimamide > thioperamide.

Clobenpropit behaves as a partial agonist, dimappit and impromidine show some agonist activity while clozapine behaves as a fall agonist. Thioperamide shows inverse agonist activity was inverse agonist. Theorem (inhibitory activity while clozapine was Histamine > N-alpha-methylhistamine > R(-)-alpha-methylhistamine > R(-)-alpha-methylhistamine behave as full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLECTIDE SEQUENCE [LARGE SCALE MRNA].
Publ H.L. III, Ikeda S.R., Aronatam R.S.;
Publ H.L. III, Ikeda S.R., Aronatam R.S.;
"CDNA clones of human proteins involved is signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
Submitted (JUL-2002) to the EMBI/GenBank/DDBJ databases.
-!- FUNCTION: The H4 subclass of histamine receptors could mediate the
histamine signals in peripheral tissues. Displays a significant
level of constitutive activity (spontaneous activity in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'Reilly M.A.; "Identification of a histamine H4 receptor on human eosinophils - Role in eosinophil chemotaxis."; "In eosinophil chemotaxis.";
                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA].

MEDLINE=21106320; PubMed=11179436;

Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J.,

Bayce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,

Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,

Bergsma D.J., Fitzgerald L.R.;

"Cloning, expression, and pharmacological characterization of a novel human histamine receptor.",

Mol. Pharmacol. 59:434-441(2001).
                                                                                                                                                                                            TISSUE-Eosinophil;
MEDLINE-21104636; PubMed=11181941;
Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,
Anthes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,
Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,
                                                                                                                                                                                                                                                                                                               Monsma F.J. Jr.;
"Cloning and characterization of a novel human histamine receptor.";
                                         Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J., Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.; "Cloning and pharmacological characterization of a fourth histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                              NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                      J. Pharmacol. Exp. Ther. 296:1058-1066(2001).
                                                                                                         expressed in bone marrow.";
                                                                                                                                Mol. Pharmacol. 59:420-426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA].
  TISSUE=Bone marrow;
                      PubMed=11179434;
                                                                                                              receptor (H4)
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EMBL; AB044934; BAB13698.1; -; mRNA.

SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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239 SASTEVPASFHSERQRRKSSLMFSSRTKANSNTIASKMGSFSQSDSVALHQREHVELLRA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 SFLEFVIPVILVAYFNMNIYWSLWKRDHLSRCQSHPGLTAVSSNICGHSFRGRLSSRRSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-palmitoyl cysteine (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Glycoprotein; Lipoprotein; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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2 (Potential).
Extracellular (Potential).
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Cytoplasmic (Potential).
Extracellular (Potential).
5 (Potential).
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7 (Potential).
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/FTId=PRO 0000069693.
Extracellular (Potential).
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                                                                                                                                                                                                                                 GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004969; F:histamine receptor activity; NAS.
InterPro; IPR000217; GPCR_Rhodpen.
InterPro; IPR000102; Histamn H4 rcpt.
PANTHER; PTHR19266:SF82; Histamnrecept_H4; 1.
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H -> R (in Ref. 1)
Q -> R (in Ref. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palmitate; Receptor; Transducer; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Potential)
                                                                                                                                                            Ensembl; ENSG0000134489; Homo sapiens
HGNC; HGNC:17383; HRH4.
mRNA.
mRNA.
mRNA.
mRNA.
                                                                                         AJ298292; CAC83493.1; -; mRNA. AY136745; AAN01271.1; -; mRNA.
AAG32052.1; -;
AAK12081.1; -;
AAK43542.1; -;
                                                                     AF325356; AAL01684.1; -;
                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
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Transmembrane
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SKWRDRRS
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X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

REDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Robar S.A., McEvan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Generation and initial analysis of more than 15,000 full-length human
RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
                        . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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EMBL; BC112148; AA112149.1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:000184; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001184; F:rhodopsin-like receptor protein signalin.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

InterPro; IPR008102; Histamn_H4_rcpt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project;
Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                      30-AUG-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                       391
                                                                                                                                                                                                                                                          390 AA.
                                                                                         361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                         sequence version 1. entry version 8.
                                                                                                                                                                                                                                                        PRELIMINARY;
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TISSUE=PCR rescued clones;
                                                                                                                                                                                                                                                                                                                                                                          Histamine H4 receptor.
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                                                                                                                                                                                                                                                        Q4G016_HUMAN
Q4G016;
                                                                                                                                                                                                                                                                                                                            30-AUG-2005,
                                                                                                                                                                                                                                                                                                                                                      21-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                     Name=HRH4;
301
                                                                                                                                                                                                                                  HIMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                               SASTEVPASFHSERQRRKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA
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Hiyama H., Kobori M., Katoh M.; Takasaki J., Kamohara M., Soga T
"Molecular cloning of monkey histamine H4 receptor.";
J. Pharmacol. Sci. 98:319-322 (2005).
-: SUBCELLULAR LOCATION: Membrane (By similarity).
-: SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                        3,
                                                                                                                                                                                                                                               Length 390;
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                                                                          PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Membrane; Receptor; Transducer;
                                                                                                                                                                                                                                                                                                      82; Indels
                                                                                                                                                                                           390 AA; 44496 MW; C986BBAE7FF912C3 CRC64;
                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                      ; Pred. No. 1.5e-90; 40; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-0CT-2005, integrated into UniProtKB/TrEMBL
11-0CT-2005, sequence version 1.
21-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15968139; DOI=10.1254/jphs.SC0050033;
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                                                                                                                                                                                                                                               66.9%; Score 1370.5;
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity 68.19
Matches 267; Conservative
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Transmembrane
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                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                        121 SYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTIT 180
                                                                                                                                                                                                                                                                                                                                                                       239 SASTEMPVSLHSERQRRKSSLMYSLRTKMNSNRIASKMGSFSQSDSVGLHQREHAELLRA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 PGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSETGSKSVWYRIAFWLQWFNSFVNPLLY 358
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                . . ; IEA
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                                                                                                                                                                                                                                                              1 MPDINSTINLSLSTRITLAFFMSLLAFAIMLGNAVVILAFVVDKNLRHRSSYFFLNLAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "cDNA cloning and characterization of porcine histamine H4 receptor.";
                                                                                                                                                                                                                                               1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKLARSLAILLSAFAI CWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Spleen;
MEDLINE=22015261; PubMed=12020829; DOI=10.1016/S0167-4781(02)00236-1;
                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oda T., Matsumoto S., Masuho Y., Takasaki J., Matsumoto M.,
Kamohara M., Saito T., Ohishi T., Soga T., Hiyama H., Matsushime H.,
Furuichi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1575:135-138 (2002).
-!- SUBCELLULAR LOCATION: Membrane (By similarity).
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR008102; Histamn_H4_rcpt.
                                                                                                                                                                                          66.3%; Score 1357.5; DB 2; Length 390; 67.6%; Pred. No. 1.3e-89; Live 42; Mismatches 82; Indels 3;
                                                                                                         PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Membrane; Receptor; Transducer;
                                                                                                                                                                 390 AA; 44463 MW; 334F219F33F209AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 PLCHKRFQKAFLKIFCIKKQPLPSPHSRSVSS 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , sequence version 1.
                                                                Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01726; HISTAMINEH4R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                        Best Local Similarity 67.69
Matches 265; Conservative
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                                                                                                                                                       Fransmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002
21-FEB-2006
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                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 RGRKCLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 RARKLARSLAILLGVFAICWAPYSLLTITRSVYPTNPFPSTAVYKFAFWLQWFNSCVNPF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                           EMBL; AB053300; BAB83078.1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004872; F:receptor IEA.

GO; GO:0004874; F:receptor activity; IEA.

GO; GO:000186; P:signal transduction; IEA.

GO; GO:0007186; P:signal transduction; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

InterPro; IPR008026; GPCR_Rhodpsn.

InterPro; IPR008026; GPCR_Rhodpsn.

InterPro; IPR008026; GPCR_Rhodpsn.

INTERPRO; IPRN080276; GPCR_Rhodpsn.

INTERPRO*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSESN--STGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNPGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELL
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Liu C., Wilson S., Kuei C., Lovenberg T.W.;

Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.

-! SUBCELLULAR LOCATION: Membrane (By similarity).

-! SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia;
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PRINTS; PR01726; HISTANINEH4R.
PROSITE; PS00237; G PROTEIN LECEP F1 1; 1.
G-protein coupled receptor; Membrane; Receptor; Transducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.7e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 SLLEFLIPILLVAYFSAHIYWSLWKREKLSRCLSHPVLPSDSSSSDHGHSCRQDPDSRAT 237
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                                                                                     EMBL; AF358858; AAK97379.1; -; mRNA.
GO; GO:0016020; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:00016020; C:membrane; IEA.
GO; GO:0001884; F:rocceptor activity; IEA.
GO; GO:0001186; P:G-protein coupled receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
GO; GO:0007186; P:G-protein foupled receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR Abdopsn.
InterPro; IPR008102; Histamn.H4 rcpt.
FANTHRR: PTRN19266; SF82; Histamnrecept_H4; 1.
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 MLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGF-STTSSSASGHLHRAGVACRTS
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21-FBB-2006, entry version 8.
Chromosome 1 SCAF15025, whole genome shotgun sequence. (Fragment).
ORFNames=GSTENG00032735001;
Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Acanthomorpha; Acanthomorpha; Acanthopterygii, Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                           Pfam; PF00001; 7tm 1; 1.

PRINTS; PR0027; GPCRRHODDSN.

PRINTS; PR01726; HISTAMINEH4R.

PROSITE; PS00237; GPOTEIN RECEP F1 1; 1.

PROSITE; PS05424; GPROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Membrane; Receptor; Transducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.4%; Score 1238; DB 2; Length 3 62.5%; Pred. No. 5.3e-81; ative 43; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 AA; 44512 MW; 51AF32FD6F1C3E4F CRC64;
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Matches 245; Conservative
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Q4RKY3 TETNG
AC Q4RKY3;
DT 19-UUL-2005, sec
DT 21-FEB-2006, ent
DF 21-FEB-2006, ent
DF 21-FEB-2006, ent
DF 21-FEB-2005, ent
DF 21-FEB-2006, ent
DF 21-FEB-2006, ent
DF 21-FEB-2006, ent
DF 21-FEB-2006, ent
DF 21-FEB-2005, ent
DF 21-FEB-20
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PubMed=15496914; DOI=10.1038/nature03025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYDRYQSVSNAVSYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSW--KNSTNTKDC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 EPGFVTEWYILTITMLLEFLLPVISVAYFNVQIYWSLWKR--------RALSRC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 YAEFYFTWYFLLSGSIFEFFTPFVSVAFFNLSIYLNIHRRIKDGGASGDDEAREQGVSKK 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, CAAE01015025, CAG10949.1; -; Genomic DNA.

GO; GO:0016021, C:integral to membrane; IEA.

GO; GO:0016020, C:membrane; IEA.

GO; GO:0004969; F:histamine receptor activity; IEA.

GO; GO:0004969; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

GO; GO:0007186; P:signal transduction; IEA.

InterPro; IPR00276; GPCR_Rhodpsn.
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Distributed under the Creative Commons Attribution-NoDerivs License
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    -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65;
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Membrane; Receptor; Transducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.8%; Score 733.5; DB 2; Length 39.7%; Pred. No. 1.3e-44; tive 60; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 AA; 46481 MW; 425E1F83C1DE28C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 431:946-957(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00001; 7tm
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354 LMIRAACSGRCVADY------WYEITFWLLWLNSAINPFLYPLCHSFRRAFSKIL 404
THMNSSITAFKVGSFWRSESAAL---RQREYAELLRGRKLARSLAILLSAFAICWAPYCL 323
                         295 -HRENSSPHGKNSRLFQPAGAGPAPDRRAQRHRLSRDKKIAKSLAIIVCIFGICWAFYTL 353
                                                    324 FTIV-----LSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKIL 375
                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21181559; PubMed=11284713; DOI=10.1042/0264-6021:3550279; Coge F., Guenin S.-P., Audinot V., Renouard-Try A., Beauverger P., Macia C., Ouvry C., Nagel N., Rique H., Boutin J.A., Galizzi J.-P.; "Genomic organization and characterization of splice variants of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
Balley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008; Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.; "Molecular cloning and characterization of a new human histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORMS 1; 3; 4; 5; 6 AND 7).
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                                                                                                                                                                                                                                                           07-MAR-2006, entry version 49.
Histamine H3 receptor (HH3R) (G-protein coupled receptor 97).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21953383; PubMed=11956964; DOI=10.1007/s007020200036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT VAL-280.
                                                                                                                                                                                                   HRH3_HUMAN STANDARD; PRT; 445 AA.
925X5H; 949KT; 956XZ; 99H4KB;
16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
16-NOV-2001, sequence version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 279:615-620(2000)
                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Pharmacol. 55:1101-1107(1999).
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99278519; PubMed=10347254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       histamine H3 receptor."
                                                                                                                                                                                                                                                                                    Name=HRH3; Synonyms=GPCR97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zirwes E.,
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor, HH4R.";
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Thalamus;
                                                                                                                                                                                                                                                                                                                                                        TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Thalamus;
                                                                                                        376 C 376
                                                                                                                                   405 C 405
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NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

NEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratasher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A patchench L., Marusia K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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B. Whiting M., Achinital analysis of more than 15,000 full-length human
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Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaeslainho M.H., Leversham M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
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Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
Swann R.M., Sycanore N., Taylor R., Thomas D.W., Thorpe A.,
Swann R.M., Sycanore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Mitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Willming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of agonist). Agonist stimulation of isoform 3 niether modified adenylate cyclase activity nor induced intracellular calcium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comment=Additional isoforms seem to exist;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 414:865-871(2001).
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                            LCVTK 379
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Q548M6;
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GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0004969; F:histamine receptor activity; TAS.
GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
GO; GO:0007269; P:neurotransmitter secretion; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
            relative expression level varies in a region-specific manner. Isoform 3 and isoform 7 are highly expressed in the thalamus, caudate nucleus and cerebellum while isoform 5 and isoform 6 show a poor expression. Isoform 5 and isoform 6 show a high expression in the amygdala, substantia nigra, cerebral cortex and hypothalamus. Isoform 7 is not found in hypothalamus or substantia
                                                                                                                     modest affinity for thioperamide, imetit, N-alpha-methylhistamine and R(-)-alpha-methyllistamine. Isoform 4 is unable to bind to iodoproxyfan while isoforms 1 and 3 bind it with high affinity. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                             nigra.
MISCELLANEOUS: Does not bind to cimetidine and tripolidine. Shows
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 various isoforms are mainly coexpressed in brain, but their
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PS50262; G PROTEIN RECEP F1 2; 1.
ive splicing; G-protein coupled receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane; Polymorphism; Receptor; Transducer; Transmembrane.
CHAIN 1 445 Histanine H3 receptor.
/FITG=PRO 000006959.
TOPO_DOM 1 39 Extracellular (Potential).
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Potential.
Extracellular (Potential)
Potential.
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Extracellular (Potential)
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/FTId=VSP_001883.
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                                                                                                                                                                                                                                                      AB019000; BAB17030.1; -; mRNA.
AJ296652; CAC51025.1; -; Genomic_DNA.
AJ278250; CAC39434.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                             EMBL; AF363791; AAK50040.1; -; mRNA. EMBL; AL078633; CAC04014.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                         EMBL, BC096840, AAH96840.1, -, mRNA. -
Ensembl, ENSG00000101180, Homo sapiens.
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EMBL; AB045369; BAB20090.1; -; mRNA.
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
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381
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10;

Gaps

93;

Indels

; Pred. No. 8.5e-44; 51; Mismatches 116;

35.3%;

Conservative

Best Local Similarity Matches 165; Conserv

Query Match

Score 722.5; DB 1; Length 445;

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191
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Ensembl; ENSGGO0001180; Homo sapiens.
GO; GO:10016021; C:integral to membrane; IEA.
GO; GO:1016020; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004969; F:histamine receptor activity; IEA.
GO; GO:0001894; F:receptor activity; IEA.
GO; GO:0001894; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR003980; H3_rcpt.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                             || :| || :| || :| || 274 RYGVGEAAVGAEAGEATLGGGGGG----GSVASPTSSSG----SSSRGTERPR-----
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LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
                                                                                                                                                                                                                          VAVWILAFLVNGPMILASDSWK-----NSTNTKDCEPGFVTEWYILTITMLLEFLLPVIS
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Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,

    -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SÜBCELLULAR LOCATION: Membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoforms of the Human Histamine H3 Receptor."; Neuropharmacology 0:0-0(2002).
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Histamine H3 receptor isoform 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 AICWAPYCLFTIVLSTYPRIERPKSVWYSIAFWLOWFNSFVNPFLYPLCHRRFQKAFWKI 374
                                                                                                                                                                                 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor: evidence for two isoforms.";
NeuroReport 11:755-759(2000).
-!- FUNCTION: The H3 subclass of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of
                                                                                                                                                                        VAVWILAFLVNGPMILASDSWK----NSTNTKDCEPGFVTEWYILTITMLLEFLLPVIS
                                                                                                                                                                                                                                                                              157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS
                                                                                                                                                                                                                                                                                                     ----WSLWKRRALSRCPSH
                                                                                                                                                                                                                                                                                                                            214 VIFFNLSÍÝLNIQRRIRLRLDGAREAAGPEPPPEAQPSPPPPGCWGCWQKGHGEAMPLH
                                                                                                                                                          18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
                                                                                                                                                                                                                                                                                                                                                                         274 RYGVGEAAVGAEAGEATLGGGGGG----GSVASPTSSSG----SSSRGTERPR----
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain,
MEDLINE=20218440; PubMed=10757514;
Tardivel-Lacombe J., Rouleau A., Heron A., Morisset S., Pillot C.,
Cochois V., Schwartz J.-C., Arrang J.-M.;
"Cloning and cerebral expression of the guinea pig histamine H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                 93;
                                                                                                          DB 2; Length 445;
                                PROSITE; PS0023'; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Membrane; Receptor; Transducer;
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eut.
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
                                                                                  445 AA; 48657 MW; 001205D765B705F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS LONG AND SHORT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9JI35; Q9JI36;
16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
16-NOV-2001, sequence version 2.
                                                                                                      35.3%; Score 722.5; DB 2; 38.8%; Pred. No. 8.5e-44; tive 51; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hystricognathi; Cavidae; Cavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry version 32.
           PRINTS; PR00237; GFCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Histamine H3 receptor (HH3R).
                                                                                                                                                                                                                                                                                                        VAYFNVOIY-----
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
Pfam; PF00001; 7tm 1; 1.
                                                                                                                      Local Similarity
Les 165; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375 LCVTK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCPQK 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10141;
                                                                       Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=HRH3;
                                                                                                                                                                                                                                                                                                                                                      216
                                                                                                                                                                                                                                                                                                                                                                                                                             319
                                                                                    SEQUENCE
                                                                                                            Query Match
                                                                                                                       Best Loca
Matches
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HRH3 CAVPO
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275 HRYGVGEAGPGAEAGEAALGGGSGAASPTSSSGSSSRGTERPR-----SLKRGSKPS 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 TGRWTFGRGLCKLWLVVDYLLCTSSVFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKM 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 VLVWVLAFILIYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 VTFFNLSIYLNIQRRTRLRLDGGAREAGPDPLPEAQSSPPQPPPGCWGCWPKGQGESMPL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HA-GFSTTSSSA-SGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILVSLRTHMNSS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAVWILAFLVNGPMILASDSWK----NSTNTKDCEPGFVTEWYLLTITMLLEFLLPVIS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 LAALMALLIVATVLGNALVMLAFVADSSLRTQNNFFLLMLAISDFLVGVFCIPLYVPYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
                                                                                      INCOLOR 135-1; Sequence=Displayed;
Name=Short; Synonyms=H3S;
IsoId=090135-1; Sequence=VSP 001880;
-!- TISSUE SPECIFICITY: Expressed widely and abundantly throughout thbrain. Highly expressed in discrete neuronal populations such as pyramidal cells in cerebral cortex or cerebellar Purkinje cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
SÜBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Print; Processis Trail; 1.

PRINTS; PRO0237; GFCRRHODOPSN.

PRINTS; PR01471; HISTAMINEH3R.

PROSITE; PS010237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

Alternative splicing; G-profein coupled receptor; Glycoprotein; Membrane; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.2%; Score 721; DB 1; Length 445; 39.8%; Pred. No. 1.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (in isoform Short)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTIG=VSP_001880.
48735 MW; BAE206A3887189A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extracellular (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histamine H3 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0000069689
                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTIG=PRO
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                                                                                                                                                                                                                                                                                                                                                   EMBL; AF267537; AAF78947.1; -; mRNA.
EMBL; AF267538; AAF78950.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR003980; H3_rcpt.
                                                                       Name=Long; Synonyms=H3L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 162; Conservative
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Name=1, Synonyms=HJL;
IsoId=09QYN8-1; Sequence=Displayed;
Name=2; Synonyms=H3S;
                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurons in brain.";
Nature 408:860-864(2000).
                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Hypothalamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor.";
Mol. Pharmacol.
                                                                                                                                                       379 K 379
                                                                                                                                                                               K 431
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216
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                         328 ASSASLEKRWKWVSQSITQR--FRLSRDKKVAKSLAIIVSIFGLCWAPYTLLMIIRAACH 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 F-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIVAQM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGNTRAVRKM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
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            ITAFKVGSFWRSESAALRQREYAELLRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 VAVWILAFLVNGPMILASDSWK----NSTNTKDCEPGFVTEWYILTITMLLEFLLPVIS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 VTFFNLSIYLNIQRRTRLRLDGAREAGGPEPPPEAQPSPPPPGCWGCWQKGHGEAMPLH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLVWVLAFLLYGPAIL --- SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85; Gaps
                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY231164; AA063757.1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:imtegral to membrane; IEA.

GO; GO:0016969; E:interamine receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

InterPro; IPR003801; H3_rcpt.
                                                                                                                                                                                                                                                                                                                                         Yao B.B., Sharma R., Cassar S., Esbenshade T.A., Hancock A.A., Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 445;
                                                                              GHCVP-DYWYETSFWILLWANSAVNPVLYPLCHYSFRRAFTKILCPQK 431
                                                              333 RIERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKILCVTK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Membrane; Receptor; Transducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 AA; 48591 MW; E79440A4EC09CA8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                   -! - SUBCELLULAR LOCATION: Membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 35.1%; Score 718.5; DB 2; al Similarity 38.7%; Pred. No. 1.7e-43; 163; Conservative 52; Mismatches 121;
                                                                                                                                                                               01-JUN-2003, integrated into UniProtKB/TrEMBL. 01-JUN-2003, sequence version 1.
                                                                                                                                                        445 AA.
                                                                                                                                                                                                                                                                                        Cercopithecidae; Cercopithecinae; Macaca.
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                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                         21-FEB-2006, entry version 15.
Histamine receptor H3.
                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                    TaxID=9544;
                                                                                                                                                       Q865E1_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane
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319 APYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKILCVT 378
                                                                                                                                                                                                                                                                                                                                                                                                                         372 APYILLMIIRAACHGHCVP-DYWYETSFWLLWANSAVNPVLYPLCHHSFRRAFIKLLCPQ 430
-----AGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILVSLRT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Corpus striatum;
MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;
Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,
Stark H., Schunack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.;
"High constitutive activity of native H3 receptors regulates histamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Figure 100 the H3 subclass of histamine receptors could mediate the FUNCTION: The H3 subclass of histamine system. Signals histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylate cyclase and displays high constitutive activity (spontaneous activity in the absence of
                                                                                   274 RYGVGEAAAGAEAGETALGGGGGGSAASPTSSSG----SSSRGTERPR-----
                                                                                                                                                                            HMNSSITAFKVGSFWRSESAALROR-----EYAELLRGRKLARSLAILLSAFAICW
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SÜBCELLULAR LOCATION: Membrane; multi-pass membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20330707; PubMed=10869375;
LOVenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
Cloning of rat histemine H3 receptor reveals distinct species
pharmacological profiles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99278519; PubMed=10347254; Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J., Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J., Huvar A., Jackson M.R., Erlander M.G.; "Cloning and functional expression of the human histamine H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLECTIDE SEQUENCE [MRNA] (ISOFORMS 1; 2; 3 AND 4).
Itadani H., Takimura T., Nakamura T., Ohta M.;
"Cloning of a novel G protein-coupled receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9QYM8; Q9QYN6; Q9QYN7; Q9QXN9;
16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
07-NAX-2000, sequence version 1.
07-NAX-2006, entry version 39.
Histamine H3 receptor (HH3R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 AA.
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GO; GO:0004969; F:histamine receptor activity; IDA.
GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; IDA.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003980; H3 rcpt.
                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP_001887.
WYETSFWLLWANSAVNPVLYPLCHYSFRRAFTKLLCPQKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQPHGSLEQCWK -> CVERLGKLEASLLLPLWMFSGRWRR
RKHVCELDVPWMFNQERQNCRGARGWIGRCGLPRPPFSVLQ
                                                    ISOId=Q9QYN8-4; Sequence=VSP 001888, VSP 001889; TISSUE SPECIFICITY: Expressed abundantly in brain, most notably throughout the thalamus, the ventromedial hypothalamus and the caudate nucleus. Isoform i is largely predominant in all tissues. MISCELLANEOUS: Proxyfan acts as a potent neutral antagonist while thioperamide, ciproxifan and FUB465 act as potent inverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPAEPROLLLPAPPGLGRWPCPACPVCTIRIWGWVVMG
                                                                                                                                                         -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poly-Ala.
N-linked (GlCNAc. . .) (Potential).
Missing (in isoform 3 and isoform 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
Alternative splicing; G-protein coupled receptor; Glycoprotein;
Membrane; Receptor; Transducer; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 445;
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Potential.
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40.2%; Pred. No. 2.3e-43;
                                                                                                                                                                                                                                                                                                                  Ensembl; ENSRNOG00000000800; Rattus norvegicus.
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IsoId=Q9QYN8-2; Sequence=VSP_001887;
                            IsoId=Q9QYN8-3; Sequence=VSP 001888;
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EMBL, AX009370; AAK02069.1; -; MENA.
EMBL, AB015646; BAA88765.1; -; MENA.
EMBL, AB015646; BAA88766.1; -; MENA.
EMBL, AB015646; BAA88768.1; -; MENA.
EMBL, AB015646; BAA88768.1; -; MENA.
                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01471; HISTAMINEH3R.
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US-09-826-509-517
US-08-727-993-9
US-08-77-993-9
US-08-722-001-14
US-08-722-001-14
US-08-20-000-582-9
US-08-20-000-582-9
US-08-20-200-585-22
US-08-20-855-22
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Sequence 2, Application US/09414010
Patent No. 6204017
GENERAL INPORMATION:
APPLICANT Behan, Jiang Xu
APPLICANT Hedrick, Joseph A.
APPLICANT Monsma, Frederick J.
APPLICANT Morse, Kelley L.
APPLICANT Worse, Kelley L.
APPLICANT Warg, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/414,010
CURRENT PILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
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299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWFNSFVNPLLY 358
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                                                                                                                    359 PLCHKRFOKAFLKIFCIKKOPLPSOHSRSVSS 390
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APPLICANT: Hedrick, Joseph A.
APPLICANT: Hedrick, Joseph A.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Morse, Kelley L.
APPLICANT: Umland, Shelby P.
APPLICANT: Umland, Shelby P.
APPLICANT: Warng, Suke
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT APPLICATION NUMBER: 090414,010
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
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Patent No. 6869776
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
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Patent No. 6613533
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Matches 267; Conservative
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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US-09-875-076-14
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LENGTH: 390
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, I-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.9%; Score 1370.5; DB 2; Length 68.1%; Pred. No. 2e-105; ive 40; Mismatches 82; Indels
                                                                                                                                CURRENT APPLICATION NUMBER: US/09/875,076 CURRENT FILING DATE: 2001-06-06
                                                                                                                                                                                                       PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/121,916
PRIOR APPLICATION NUMBER: 60/121,916
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-02-26
PRIOR PELING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR PELING DATE: 1999-05-28
PRIOR PELING DATE: 1999-05-29
PRIOR PELING DATE: 1999-00-29
PRIOR PELING DATE: 1999-00-10
PRIOR PELING DATE: 1999-00-10
PRIOR PELING DATE: 1999-00-10
PRIOR PELING DATE: 1999-10-01
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/417,044
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                                                                                                            FILE REFERENCE: ARENO050
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368 GLCWAPYTLIMIIRAACHGHCVP-DYWYETSFWLLWANSAVNPVLYPLCHHSFRRAFTKL 426
                           --- WSLWKRRALSRCPSH 215
                                                                    214 VTFFNLSIYLNIQRRTRLRLDGAREAAGPEPPPEAQPSPPPPGCWGCWQKGHGEAMPLH 273
                                                                                                               -----AGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILV 263
                                                                                                                                                                                                 264 SLRTHMNSSITAFKVGSFWRSESAALRQR-----EYAELLRGRKLARSLAILLSAF 314
                                                                                                                                                                                                                          SIMPLE SELEKENKAVSOSFTQRFRLSRDRKVAKSLAVIVSIF 367
                                                                                                                                                                                                                                                                                   315 AICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKI 374
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                                                                                                                                                      274 RYGVGEAAVGAEAGEATLGGGGGG----GSVASPTSSSG----SSSRGTERPR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.3%; Score 722.5; DB 2; Length 38.8%; Pred. No. 8.8e-52; tive 51; Mismatches 116; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33.505
REFERENCE/DOCKET NUMBER: MNI-032CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/165,543 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
RATIOR APPLICATION NUMBER: 09/042,780
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 165; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STRET: 28 State Street
CIT: Boston
STATE: USA
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                                                                                                                                                                                                                                                                                      361 PLCHRRFQKAFWKILCVTKWPALSQ-NQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08985090
Patent No. 5885893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445 amino acids
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                          JS-08-985-090-2
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	QY 264 SLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRGRKLARSLAILLSAF 314 :         :         :	QY 315 AIGWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFOKAFWKI 374 :          ::	Oy 375 LCVTK 379             Db 427 LCPQK 431	35.	4.26 E	4 P 4 P 1	; FILE REFERENCE: JWW ; CURRENT APPLICATION NUMBER: US/09/642,855 ; CURRENT PILLING DATE: 2000-08-21 ; PRIOR APPLICATION NUMBER: 09/167,354 ; PRIOR FILLING DATE: 1998-10-06	NUMBER SOFTWAI SEQ ID 1 LENGTI	; TYPE: PRT ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE US-09-642-855-7	Query Match 35.3%; Score 722.5; DB 2; Length 445; Best Local Similarity 38.8%; Pred. No. 8.8e-52; Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;	Qy 18 LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLXIPHVL 77	Oy 78 F-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIVAQM 136	Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKM 156 Qy 137 VAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTITMLLEFILPVIS 191		214 VTFFNLSIYLNIQRRTRLRLDGAREAAGPEPPPEAQPSPPPPGCWGCWQKGHGEAMPLH	Qy 216AGFSTTSSSASGHLHRAQVACRTSNPGLKESAANHSESFKKKSSLLV 263	SIRTHMNSSITAFKVGSFWRSBSAALRQREYAELLRGRKLARSLAILLSAF :	Db 319SLKRGSKPSASSASLEKRMKOVSQSFTQRFRLSRDRKVAKSLAVIVSIF 367	368
	Qy 137 VAVWILAFLVNGPMILASDSWKNSTNTKDCEPGFVTEWYILTITMLLEFLIPVIS 191 5	Qy 192 VAYENVQIY	Qy 216AGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILV 263  Db 274 RYGVGEAAVGEAAGEATLGGGGGGGSVASPTSSSGSSSRGTERPR 318	Qy 264 SLRTHMNSSITAFKVGSFWRSESAALRQREYAELLRGRKLARSLAILLSAF 314 :	Qy 315 AICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFUNPFLYPLCHRRFQKAFWKI 374	Qy 375 LCVTK 379 	RESULT 6 US-09-167-354-7 US-09-167-354-7 Sepent No. 613659	; GENERAL INFORMATION: ; APPLICANT: Lovenberg, Timothy ; APPLICANT: Frlander, Mark ; APPLICANT: Pyati, Jayashree	; APPLICANT: Huvar, Arne ; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3 ; TITLE OF INVENTION: SUBTYPE ; FILE REFERENCE: JWW ; CURRENT APPLICATION NUMBER: US/09/167,354A	; CURRENT FILING DATE: 1998-10-07; NUMBER OF SEQ ID NOS: 8; SOGTWARE: PatentIn Ver. 2.0; SEQ ID NO 7		; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE US-09-167-354-7	Query Match 35.3%; Score 722.5; DB 2; Length 445; Best Local Similarity 38.8%; Pred. No. 8.8e-52; Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps 10;	18 LAFLMSSFAFAIMVGNAV	78 F-WWNFGSGICMFWLITDYLLCTASVXNIVLISYDRYQSVSNAVSYRAQHTGIMKIVAQM	Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRM 156 Qy 137 VAVWILAFLVNGFWILASDSWKNGTNTKDCEPGFVTEWYILTITMLLEFLLPVIS 191	Db 157 LLVWVLAFLLYGPAILSWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 213	Qy 192 VAYPNVQIY	216AGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILV

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375 LCVTK 379
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SENERAL INFORMATION:
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Patent No. 6437100

GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Evlander, Mark
APPLICANT: Havar, Arne
APPLICANT: Pyati, Jayashree
APPLICANT: Pyati, Jayashree
TITLE OF INVENTION: SUBTYPE
FILE REFRENCE: ORT1290
CURRENT APPLICATION NUMBER: US/09/642,514
CURRENT APPLICATION NUMBER: US 09/167,154
PRIOR APPLICATION NUMBER: US 09/167,154
PRIOR APPLICATION NUMBER: US 09/167,154
SRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.0
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35.3%; Score 722.5; DB 2; Length 445;
Best Local Similarity 38.8%; Pred. No. 8.8e-52;
Matches 165; Conservative 51; Mismatches 116; Indels 93; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE US-09-642-514-7
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Patent No. 6855560
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ORGANISM: Artificial Sequence
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                                  375 LCVTK 379
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97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGDTRRAVRKM 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 LLVWVLAFLLYGPAIL --- SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 213
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37 LAALMALLIVATVICGNALVMLAFVADSSLRTQNNFFLILNLAISDFLVGAFCIPLYVPYVL
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APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Extander, Mark
APPLICANT: Extander, Mark
APPLICANT: Payet, Jayashree
APPLICANT: Payet, Jayashree
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/642,852
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: 09/167,354
PRIOR APPLICATION NUMBER: 09/167,354
PRIOR FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 445
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APPLICANT: PADLOGY, ROLF
TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A]PYRAZINES,
TITLE OF INVENTION: OUTCAHYDROPYRAZINO[1,2-A]PYRAZINES,
TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A]AZEPINES
TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A]AZEPINES
CURRENCE: 6483.200-US
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: US/10/453,106
PRIOR APPLICATION NUMBER: US 60/387,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE US-09-642-852-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.3%; Score 722.5; DB 2; Length 4 Best Local Similarity 38.8%; Pred. No. 8.8e-52; Matches 165; Conservative 51; Mismatches 116; Indels
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ORGANISM: Artificial Sequence
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Length 449;

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Matches 165; Conservative
                  Best Local Similarity 50.0
Matches 165; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-01-02
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFFWARE: FastSEQ for Windows Version 4.0
LENGTH: 449
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                                                                                                                                                                                                                  y Match 35.3%; Score 722.5; DB 2; Length 445; Local Similarity 38.8%; Pred. No. 8.8e-52; Conservative 51; Mismatches 116; Indels 93; Gaps
              PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863 PRIOR FILING DATE: 2002-06-06 NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin version 3.2 SEQ ID NO 1 LENGTH: 445
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Patent No. 6812339
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PRIOR FILING DATE: 2002-06-07
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US-09-949-016-10930
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                                     Gaps
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35.3%; Score 722.5; DB 2; Length 38.8%; Pred. No. 8.9e-52; ive 51; Mismatches 116; Indels
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Nakamura, Takao
Kobayashi, Masahiko
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214 VTFFNLSIYLNIORRTRLRLDGAREAGGPEPPPEAQPSPPPPGCWGCWQKGHGEAMPLH 273
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      ----WSLWKRRALSRCPSH 215
                                                                                         216 -----AGFSTTSSSASGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILVSLRT 267
                                                                                                                                                                                                                                                              319 APYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKILCVT 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09165543
Patent No. 6091545
PARENT NO. 6091545
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.0%; Score 716.5; DB 2
40.2%; Pred. No. 2.8e-51;
tive 54; Mismatches 128
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REGISTRATION NUMBER: 33,505
REGISTRATION NUMBER: MNI-032CP
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATHOR APPLICATION NUMBER: 09/042,780
FILING DATE:
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IBM PC compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
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amino acid
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STATE: Massachusetts
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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      192 VAYFNVQIY
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US-09-165-543-5
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                                                                F-NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIVAQM 136
                                                                                                                                                   137 VAVWILAFLVNGPMILASDSWK----NSTNTKDCEPGFVTEWYILTITMLLEFLLPVIS 191
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LAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPLYIPHVL
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APPLICANT: PESCHKE, BEING
APPLICANT: PESCHKE, BEING
APPLICANT: PESCHKE, BEING
TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A] PYRAZINES,
TITLE OF INVENTION: OCTAHYDROPYRAZINO[1,2-A] PYRAZINES
TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A] PYRAZINES
TITLE REFERENCE: 6483.200-05
FILE REFERENCE: 6483.200-05
FRIOR APPLICATION NUMBER: US 60/387,047
PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
SPRIOR FILING DATE: 2002-06-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VERSION 3.2
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Patent No. 6906060
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                                               137 VAVWILAFLVNGPMILASDSWK----NSTNTKDCEPGFVTEWYILTITMLLEFLLPVIS 191
                                                                                        157 ALVWVLAFLLYGPAIL---SWEYLSGGSSIPEGHCYAEFFYNWYFLITASTLEFFTPFLS 213
                                                                                                                                       192 VAYFNVQIYWSLWKRRAL----LH 230
                                                                                                                                                                                     214 VIFFNLSIYLNIQRRTRLRLDGGREAGPEPPDAQPSPPPAPPSCWGCWPKGHGEAMPLH 273
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274 RYGVG--EAGPGVEAGEAALGGGSGGGAAASPTSSSGSSSRGTERPR-----SLKRGS 324
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TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
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CURRENT APPLICATION NUMBER: US/09/891,053
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/JP99/07280
PRIOR APPLICATION NUMBER: PCT/JP98/05967
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: US/09/806967
PRIOR APPLICATION NUMBER: US/09/806967
PRIOR PILING DATE: 1998-05-25
NUMBER OF SEQ ID NOS: 26
SEQ ID NOS: 26
SEQ ID NO 25
SEQ ID NO 25
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APPLICANT: Nakamura, Takao
APPLICANT: Kobayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yusuke
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US-10-626-126-8

US-10-626-445-9

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US-09-12-216-2

US-09-812-216-2

US-09-876-25-14

US-09-876-25-14

US-09-876-25-14

US-09-876-25-14

US-10-625-567A-629

US-10-272-983-14

US-10-349-253A-2

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APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
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TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
TITLE OF INVENTION NUMBER: 09/109,849
PRIOR FILLING DATE: 2001-02-22
PRIOR FILLING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
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100.0%; Pred. No. 6.8e-180;
ive 0; Mismatches 0;
                         US-10-756-149-4702
US-10-723-955-14
US-10-723-955-14
US-10-290-078-27
US-10-686-421-6
US-10-626-126-10
US-10-626-126-10
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US-10-125-126-12
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Best Local Similarity
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Best_Local Similarity 84.78
Matches 331; Conservative
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ORGANISM: Rattus rattus
                                                                                                                 ORGANISM: Mus musculus
                                                              SEQ ID NO 8
LENGTH: 391
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US-10-626-445-9
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                                                                                        Sequence 8, Application US/10626126
Publication No. US20050074770A1
GENERAL INFORMATION:
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DATE: 2003-07-23
CURRENT APPLICATION NUMBER: US/10/626,126
CURRENT APPLICATION NUMBER: 09/790,849
PRIOR APPLICATION NUMBER: 60/208,260
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
PRIOR SPLICATION NUMBER: 60/208,260
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
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APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0034
CURRENT APPLICATION NUMBER: US/10/626,398
CURRENT FILING DATE: 2003-07-23
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100.0%; Pred. No. 6.8e-180;
ive 0; Mismatches 0;
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361 PLCHRRFQKAFWKILCVTKWPALSQNQSVSS 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 391; Conservative
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APPLICANT: Lovenberg, Timothy
APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0032
CURRENT APPLICATION NUMBER: US/10/626,445
CURRENT FILING DATE: 2003-07-23
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
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84.7%; Pred. No. 4.7e-151;
tive 17; Mismatches 43; Indels
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PRIOR APPLICATION NUMBER: 09/790,849
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/208,260
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
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APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
TILE REFERENCE: PRO 1034
CURRENT APPLICATION NUMBER: US/10/626,398
CURRENT FILING DATE: 2003-07-23
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SEQ ID NO 9.
                                                                  61 DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV 120
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Best Local Similarity 84.7%; Pred. No. 4.7e-151;
Matches 331; Conservative 17; Mismatches 43;
                                                                                                                             PLCHRRFQKAFWKILCVTKWPALSQNQSVSS 391
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ORGANISM: Rattus rattus
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US-09-812-216-2
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Publication No. US20050074770A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAB Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE: PRD-0033
CURRENT APPLICATION NUMBER: US/10/626,126
CURRENT FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: 09/790,849
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
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                                                                                          61 DFFVGVISIPLYIPHTLENWNPGSGICMFWLITDYLLCTASVYSIVLISYDRYQSVSNAV 120
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DFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVANAV
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84.7%; Pred. No. 4.7e-151;
live 17; Mismatches 43; Indels
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Best Local Similarity 84.79
Matches 331; Conservative
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LENGTH: 391
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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                                                                                       TYPE: PRT
ORGANISM: Homo sapien
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APPLICANT: Li, Saleong
APPLICANT: Li, Saleong
APPLICANT: Alchalovich, David
APPLICANT: Zhu, Yuan
TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
FILE REFERENCE: GP70655-2C1
CURRENT APPLICATION NUMBER: US/09/910,411
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/693,761
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.9%; Score 1370.5; DB 3
Best Local Similarity 68.1%; Pred. No. 1.8e-117,
Matches 267; Conservative 40; Mismatches 82,
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                    APPLICANT: Laz, Thomas M.
APPLICANT: Morsem, Frederick J. Jr.
APPLICANT: Morsem, Frederick J. Jr.
APPLICANT: Worse, Kelley L.
APPLICANT: Unland, Shelby P.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
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Patent No. US20020137054A1
    Hedrick, Joseph A.
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APPLICANT: Fitzgerald, Laura
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SEQ ID NO 2
LENGTH: 390
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ORGANISM: Homo sapiens
US-09-812-216-2
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US-09-910-411-2
    APPLICANT:
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61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
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                                                                                    3; Gaps
        DB 3; Length 390;
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FILE REFERENCE: AREN0050
                                                                                    82; Indels
Ouery Match 66.9%; Score 1370.5; DB 3; Best Local Similarity 68.1%; Pred. No. 1.8e-117; Matches 267; Conservative 40; Mismatches 82;
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CURRENT PELING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/417, 044
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123, 946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/133, 949
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR PRILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136, 436
PRIOR PRILING DATE: 1999-05-28
PRIOR PRILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136, 439
PRIOR PRILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136, 567
PRIOR PRILING DATE: 1999-05-28
PRIOR PRILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136, 567
PRIOR PRILING DATE: 1999-05-28
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61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASVYNIVLISYDRYLSVSNAV 120
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                                         PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: 60/11,448
PRIOR APPLICATION NUMBER: 60/156,653
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/156,555
PRIOR APPLICATION NUMBER: 60/156,534
PRIOR PILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-00-19
PRIOR FILING DATE: 1999-10-01
PRIOR PRICATION NUMBER: 60/157,294
PRIOR PELING DATE: 1999-10-01
PRIOR PELING DATE: 1999-10-01
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PRIOR FILING DATE: 1999-10-01
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US-09-876-252-14
Sequence 14, Application US/09876252
Fublication No. US20030018182A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Chalmers, Derek T.
APPLICANT: Lowitz, Kevin P.
                           60/137,131
1999-05-28
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| APPLICANT: Lib. 1-1...
| APPLICANT: Lib. 2-1...
| APPLICANT: Chen, Month Houng T. APPLICANT: APPLICANT: MONTHS: 10.0.10.600
| MATCH APPLICANT: MONTHS: 10.0.10.600|
| MATCH APPLICANT: MONTH
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Sequence 6, Application US/09891138A; Publication No. US20030083245A1 GENERAL INFORMATION: APPLICANT: Lin, Daniel Chi-Hong
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 68.19
Matches 267; Conservative
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APPLICANT: Lind, Cabriel
APPLICANT: Sejlitz, Torsten
APPLICANT: Wogeli, Cabriel
APPLICANT: Wood, Linda S.
TITLE OF INVENTYON: No. US20030032784Alel G Protein-Coupled Receptors
FILE REFERENCE: 00231regUs
CURRENT APPLICATION NUMBER: US/09/852,165
CURRENT FILING DATE: 2001-05-08
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 390
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                                                                                                                            1 MPDINSTINLSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDKNLRHRSSYFFLNLAIS
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                                                                                                         1 MSESNSTGILPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAIS
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                                          DB 3; Length 390;
                                                                         82; Indels
                                       Query Match 66.9%; Score 1370.5; DB 3 Best Local Similarity 68.1%; Pred. No. 1.8e-117; Matches 267; Conservative 40; Mismatches 82;
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Best Local Similarity 68.1%
Matches 267; Conservative
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, ORGANISM: Homo sapiens
US-09-852-165-2
; OKGANISM: AC
US-09-876-252-14
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US-09-852-165-2
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APPLICANT: Zhao, Jiagang
APPLICANT: Chen, Jin-Long
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. US20030083245Alel Receptors
FILE REFERENCE: 018781-006210US
CURRENT APPLICATION NUMBER: US/09/891,138A
CURRENT FILING DATE: 2001-06-25
PRIOR FILING DATE: 2000-06-23
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, I-Lin
ITILE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REPERENCE: ARENGOSO
CURRENT FILING DATE: 2002-10-17
FRICH APPLICATION NUMBER: US/09/417,044
PRIOR PELICATION NUMBER: 00/109,213
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR PILING DATE: 1999-02-16
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PELICATION NUMBER: 60/123,946
PRIOR PILING DATE: 1999-03-12
PRIOR PELING DATE: 1999-03-12
PRIOR PELING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PELING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-05-28
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                                                                                                                                                                                                66.9%; Score 1370.5; DB 4; 68.1%; Pred. No. 1.8e-117; cive 40; Mismatches 82;
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Publication No. US20030148450A1
GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                    Matches 267; Conservative
                                                                                                TYPE: PRT
CRGANISM: Homo sapiens
US-10-225-567A-629
                                                                                                                                                                                                                          Best Local Similarity
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                                                 SEQ ID NO 629
LENGTH: 390
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APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR PILING DATE: 2000-12-19
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                                                                                                                                                                 Sequence 2, Application US/10052193
; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; ATTLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; TILE REPERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT PILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 2.
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                            PLCHRRFOKAFWKILCVTKWPALSQ-NOSVSS 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 1999-05-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 390
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CORGANISM: Homo sapiens
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APPLICANT: Healy, Alleen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 14717, 9941, 19310, c
FILE REFERENCE: MPIZONI-280PIRCPLOWNIM
CURRENT APPLICATION NUMBER: US 10/242,505A
CURRENT FILING DATE: 2005-10-03
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
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2935, Ap
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2412, App 1,
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US-10-511-937-2435
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US-11-257-851A-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo Sapiens
       RESULT 1
US-11-242-505A-27
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188 PVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSNPGLKESA 247
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APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Sosenbers, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 50661200104
CURRENT APPLICATION NUMBER: U5/10/511,937
CURRENT PILING DATE: 2004-10-19
FRIOR PELING DATE: 2003-04-24
FRIOR FILING DATE: 2003-04-24
FRIOR FILING DATE: 2002-04-24
FRIOR APPLICATION NUMBER: US 10/131,831
FRIOR PRICATION NUMBER: US 10/325,899
FRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ 1D NOS: 3117
SOFTWARE: PATENTIN VEXBION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2990, Application US/10511937; Publication No. US20060088836A1; GENERAL INFORMATION:
                                                   212 PLCVVLF----VYWKIYKAA----
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Fry, Kirk
Woodward, Robert
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     368 QKAF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 NSAF 349
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US-10-511-937-2990
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APPLICANT: Venkatesbwarlu, Karicheti
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: G41, 260, 55099, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 641, 260, 55099, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: MPIO2-012PIRNM OMNI
CURRENT APPLICATION NUMBER: US/11/302,678
PRIOR APPLICATION NUMBER: US/10/345,680
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                                                                                    239 SASTEVPASFHSERRRKKSSLMFSSRTKMNSNTIASKMGSFSQSDSVALHQREHVELLRA 298
                                                                                                                                                                                                                               76 VLF--NWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIV 133
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                                                                                                                                                                                       301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 IGFLVAATFAWNLLV-----LATILRVRTFHRVPHNLVASMAVSDVLVAALVMPLSLVH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 AQ-MVAV-WILAFLVNGPMILASDSWKNSTNTKDC----EPGFVTEWYILTITMLLEFLL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 LAFLM-SSFAFAIMVGNAVVILAFVVDRNLRHR-SNYFFLNLAISDFLVGLISIPLYIPH
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                                                                                                                                                                                                                                                                                                                                                                       359 PLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS 390
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PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/349,511
PRIOR APPLICATION NUMBER: US 60/360,500
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-08-17
PRIOR FILING DATE: 2002-08-17
PRIOR APPLICATION NUMBER: US 60/419,986
PRIOR FILING DATE: 2002-10-21
PRIOR PRIOR DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
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Best Local Similarity 24.5%
Matches 89; Conservative
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LENGTH: 357
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                                                                                                 EYAELLRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFN 352
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Sequence 3, Application US/11305477

Publication No. US20060099687A1

Publication No. US20060099687A1

APPLICANT: Glucksmann, Maria A.

TITLE OF INVENTION:

FILE REFERENCE: 015800/169197

CURRENT PAPLICATION NUMBER: US/11/305,477

CURRENT FILING DATE: 1098-09-02

FRIOR APPLICATION NUMBER: US/09/145,745

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Unknown Organism:Transmembrane OTHER INFORMATION: Receptor of the Rhodopsin Superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.8%; Score 283; DB 7; Length 269; Best Local Similarity 20.5%; Pred. No. 1.3e-17; Matches 73; Conservative 61; Mismatches 108; Indels 114;
                                 239 --VPRTPRPGV-ESADSRRLATKHSRKALKASL
                                                                                                                                                                                                                              353 SFVNPFLYPLCHRRFOKAFWKILCVTKWP 381
                                                                                                                                                                                                                                                                    313 STMNPIIYPLFMRDFKRALGRFLPCPRCP 341
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Publication No. US20060105393A1
GENERAL INFORMATION:
APPLICANT: APFEL, CHRISTIAN
APPLICANT: ENDERLE, THILD
APPLICANT: ZOFFMANN, SANNAH JENSEN
APPLICANT: PENSKI, MIREILLE
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TYPE: PRT
ORGANISM: Unknown
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US-11-255-699-4
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APPLICANT: Mileennium Pharmaceuticals, Inc.
APPLICANT: Mileennium Pharmaceuticals, Inc.
APPLICANT: Mileennium Pharmaceuticals, Inc.
APPLICANT: Mileennium Pharmaceuticals, Inc.
APPLICANT: Wenkatewarlu, Karichti
TITLE OF INVENTION: WENCHOCKAL 108026, 1318, 559, 34021, 44099, 25278,
TITLE OF INVENTION: UNCLOCATCAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
CURRENT PILING DATE: 2005-12-14
PRIOR FILING DATE: 2002-01-18
PRIOR PLING DATE: 2002-03-15
PRIOR PLING DATE: 2002-03-15
PRIOR PLING DATE: 2002-03-15
PRIOR PLING DATE: 2002-03-15
PRIOR PLING DATE: 2002-03-15
PRIOR PLING DATE: 2002-04-19
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PRIOR PLING DATE: 2002-10-21
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                                     :|| :: || || || || || || 234 VILAAVMGAFIICWFPY--FTAFVYRGIRGDDAINEVLEAIVLMIGYANISALNPIILYAAL 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                        Sequence 41, Application US/11302678 Publication No. US20060088881A1 GENERAL INFORMATION:
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292 NRDFRTGYQQLFC 304
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Best Local Similarity 24.4%
Matches 95; Conservative
                                                                                                                                364 HRRFQKAFWKILC 376
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US-11-302-678-41
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LENGTH: 440
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ORGANISM: Homo Sapiens
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US-11-242-505A-18
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                                                                 Query Match
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TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: 14385, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
TITLE OF INVENTION: 14385, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
TITLE OF INVENTION: WIMBER: US/11/242, 505A
CURRENT APPLICATION NUMBER: US/10/290, 078
PRIOR FILING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 ASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIVAQMVAVWILAFLVNGPMILASDSWKN 159
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                                                                                                                                                                                                                                                                                                                                   61; Mismatches 124; Indels 128; Gaps
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                                                                                                                                                                                                                                                                                           13.0%; Score 267; DB 7; Length 465; 23.3%; Pred. No. 6e-16;
TITLE OF INVENTION: LIGAND-RECEPTOR TRACKING ASSAYS FILE REFERENCE: 22817
FILE REPERENCE: 22817
CURRENT APPLICATION NUMBER: US/11/255,699
CURRENT FILING DATE: 2005-10-21
PRIOR APPLICATION NUMBER: EP 04105285.3
PRIOR PILING DATE: 2004-10-25
WUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.3
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LENGTH: 403
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LENGTH: 465
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72 YIPHVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAV-SYRAQHTGIM 130
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                                                                                                                                           10 LPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISI 69
                                                                                                                                                                              38 MPICATYLLIFVVGA-----VGNGLTCLVILRHKAMRTPTNYYLFSLAVSDLLVLLVGL 91
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ch 11.5%; Score 236.5; DB 7; Length 403; 1 Similarity 21.4%; Pred. No. 2.2e-13; 89; Conservative 62; Mismatches 114; Indels 151; Gaps
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22.0%; Pred. No. 1.5e-11;
tive 60; Mismatches 136; Indels 95; Gaps
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APPLICANT: ENDERLE, THILO
APPLICANT: ZOFFMANN, SANNAH JENSEN
APPLICANT: PENSKI, MIRELLLE
TITLE OF INVENTION: LIGAND-RECEPTOR TRACKING ASSAYS
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CURRENT APPLICATION NUMBER: US/11/255,699
CURRENT FILING DATE: 2005-10-21
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PRIOR FILING DATE: 2004-10-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/11255699; Publication No. US20060105393A1; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
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ORGANISM: Homo sapiens
                                         Best Local Similarity
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QY 71 LYIPHULEN-WNFGSGICMFWLITDYLLCTASYYNIVLISYDRYGSVSNAVSYRAQ 125	Db 234 AKP	RESULT 10  US-11-255-699-2  Sequence 2, Application US/11255699  Publication No. US20060105333A1  GENERAL INFORMATION: APPLICANT: APEL, CHRISTIAN APPLICANT: COFFMANN SANNAH JENSEN APPLICANT: PENSEL, THILO APPLICANT: LIGAND-RECEPTOR TRACKING ASSAYS FILE REFREENCE: 22817 CURRENT FILING DATE: 2005-10-21 PRIOR APPLICATION NUMBER: EP 04105285.3 PRIOR APPLICATION NUMBER: EP 04105285.3 PRIOR APPLICATION NUMBER: BD 04105285.3  PRIOR APPLICATION NUMBER: D04-10-25 NUMBER OF SEQ 1D NOS: 11 SOFTWARE: Patentin version 3.3  LENGTH: 366  TYPE: PRT  ORGANISM: Homo sapiens	10.1%;   Score 206.5;   DB 7;   Length 366;	Db 211 TVMVWVSSIFFFLPVFCLTVLYSLIGRKLWRR
157 KLASAAAMVLSLCMSLPLLVFADVQEGGTCNASWPEPVGLMGAVFIIYTAVLGFFAPL 214   0	Qy       367 FQKAFWKILCVTK 379         Db       311 FRQSFQKVLCLRK 323         RESULT 9       US-11-312-958-24         i Sequence 24, Application US/11312958       Publication No. US20060100152A1	GENERAL INFORMATION: APPLICANT: Milennium Pharmaceuticals, Inc. APPLICANT: Rosenfeld, Julie Beth APPLICANT: Rosenfeld, Julie Beth APPLICANT: Silos-Santiago, Inmaculada TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636, TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373, TITLE OF INVENTION: 27410, 33260, 619, 15986, 69112, 2158, 224, 615, 9569 OR TITLE OF INVENTION: 13424 MOLECULES FILE REFERENCE: MAID 2-027 PROMORIM TITLE OF INVENTION: 13424 MOLECULES FILE REFERENCE: MAID 2-027 PROMORIM CURRENT APPLICATION NUMBER: US/11/312,958 CURRENT APPLICATION NUMBER: US/0769,022 PRIOR PRILING DATE: 2002-02-28 PRIOR FILING DATE: 2002-02-28 PRIOR FILING DATE: 2002-04-04 PRIOR FILING DATE: 2002-04-04 PRIOR FILING DATE: 2002-04-16 PRIOR FILING DATE: 2002-04-16 PRIOR FILING DATE: 2002-04-16 PRIOR PRILING DATE: 2002-04-16	002-05-03 WBER: US 602-05-13 WBER: US 60 W	Indels SNYFFLNLA     ::

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70 PLYIPHVLFN-WNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSN---AVSYRAQ 125
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                                                                                                                               244 KESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALROREYAELLRGRKL 303
                                                           -----MIGDVTTEQYFALRRKK-----KKT 290
                                                                                                        304 ARSIAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFVNPFLYPLC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LPPAAQVPLAFLMSSFAFAIMVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.0%; Score 204; DB 7; Length 380;
19.9%; Pred. No. 1.3e-10;
tive 68; Mismatches 131; Indels 102;
                                                                                                                                                                                                                            364 HRRFQKAFWKILCVTKWPALSQNQSVSS 391
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                  ; Sequence 20, Application US/11302678; Publication No. US20060088881A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75; Conservative
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Best Local Similarity
Matches 75; Conserva
                                                                                                                                                                                                                                                                                                                                  US-11-302-678-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 380
TYPE: PRT
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APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: MATHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PATH AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION: 12316, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
TITLE OF INVENTION: 19424 MOLECULES
FILE REPERENCE: MPLOS-OZPIRNOWIM
CURRENT APPLICATION NUMBER: US/11/312,958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 YIAVIWTWATPFSLPHAICQKLFTFKYSEDIVRSLCLPDFPEPADLFWKYLDLATFILLY 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 HVLFNWNFGSGICMFWLITDYLLCTASVYNIVLISYDRYQSVSNAVSYRAQHTGIMKIVA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 QMVAVWILAFLVNGPMILASD--SWKNSTN--TKDCEPGFVTE----W-YILTITMLLEF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 LLP--VISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRTSNPGL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- 270
259 -----KQTVKMLAVVVPAFILCWLP---FHVGRYLFSKSFEFGSLEIAQISQYCNLVSF 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 FVNSTWIFGKGMCHVSRFAQYCSLHVSALTLTAIAVDRHQVIMHPLKPR---ISITKGVI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 AFLMSSFAFAI----MVGNAVVILAFVVDRNLRHRSNYFFLNLAISDFLVGLISIPL-YIP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
10.1%; Score 206; DB 7; Lengtn 4.2;
Best Local Similarity 19.8%; Pred. No. 1e-10;
Matches 77; Conservative 66; Mismatches 147; Indels 98; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior Application data removed - See File Wrapper or PALM.
                                                                                             | : :: : | | | : ::: | ::: | 338
                                                                    347 WLQWFNSFVNPFLYPLCHRRFQKAFWKIL 375
                                                                                                                                                                                                                                                                                            APPLICANT: Millennium Pharmaceuticals, Inc.
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PRIOR PELLING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR PELLING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-04-04
PRIOR PILING DATE: 2002-04-04
PRIOR PILING DATE: 2002-04-16
PRIOR PILING DATE: 2002-04-16
PRIOR PLING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373,717
PRIOR FILING DATE: 2002-04-19
PRIOR PLING DATE: 2002-05-03
PRIOR PLING DATE: 2002-05-03
PRIOR PLING DATE: 2002-05-03
PRIOR PLING DATE: 2002-05-03
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 423
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PRIOR FILING DATE: 2002-06-06
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Publication No. US20060100152A1
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                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                     US-11-312-958-12
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QY         180 -TMLLEFLLFVISVAYFNVQIYWSLWKRRALSRCPSHAGFSTTSSSASGHLHRAGVACRT 238           Db         229 CVFIFAFVIPVLII	Qy 281 FWRSESAALRQREYAELLRGRKLARSLAILLSAFAICWAPYCLFTIVLSTYP     :	-LSTYP 332   DLGALA 287
Qy 239 SNPGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGSFWRSESAALRQREYAELL 298	Qy 333 RTERPKSVWYSIAFWLQWFNSFVNPFLYPLCHRRFQKAFWKIL 375	
248LKSVRLLSGSREKDRNL	288 RNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMMLL	
299 RGRKLARSLAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWFNSFV	RESULT 14	
Db 270RRITRLVLVVVAVEVVCMTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSSL 325	US-10-511-937-2931 ; Sequence 2931, Application US/10511937 . Bublication No. TECONGENESSEN	
326 NPILYAFLDENFKRCF	; GENERAL INFORMATION: ; APPLICANT: EXPRESSION DIAGNOSTICS, INC. · ADDIATOMY: Mohidemuth law	
RESULT 13	APPLICANT: Fry, Kirk, APPLICANT: Rry, Kirk, APPLICANT: Woodward, Robert	
OS-10-211-397-2303; Sequence 2505, Application US/10511937 ; Publication No. US20060088836A1	; APPLICANT: LY, NGOC, James ; APPLICANT: Morris, MacDonald	
; GENERAL INFORMATION: ; APPLICANT: EXPRESSION DIAGNOSTICS, INC. ; APPLICANT: Wohldemuth, Jav	; APPLICANT: Rosenberg, Steven ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING ; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION	
	; FILE REFERENCE: 506612000104 ; CURRENT APPLICATION NUMBER: US/10/511,937	
	; CURRENT FILING DATE: 2004-10-19 ; PRIOR APPLICATION NUMBER: PCT/US2003/012946	
44	; PRIOR FILING DATE: 2003-04-24 ; PRIOR PAPLICATION NUMBER: US 10/131,831	
) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING ) TITLE OF INVENTION: ADD MONITORING TRANSPLANT REJECTION  TITLE OF INVENTION: ADD MONITORING TRANSPLANT REJECTION	; PRIOR FILING DATE: 2002-04-24; PRIOR APPLICATION NUMBER: US 10/325,899	
NE	FALLOR FILLING DALE: ZOUZ-12-ZO ; NUMBER OF SEQ ID NOS: 3117	
; CURKEN! FILING DAIL: 2004-10-19 ; FRIOR APPLICATION NUMBER: PCT/US2003/012946 : PRIOR FILING DATE: 2003-04-24	2931 368	
; PRIOR APPLICATION NUMBER: US 10/131,831 ; PRIOR FILING DATE: 200-204-24 ; PRIOR APPLICATION NUMBER: US 10/325,899	; TYPE: PRT ; ORGANISM: Homo sapiens US-10-511-937-2931	
FRIOR FILING DATE: 2002-12-20 FINDRER OF SEQ ID NOS: 3117 FORMARIAN OF SEQ ID NOS: 3117	Query Match 9.9%; Score 203; DB 6; Length 368;	
Facencin version 2505	ocai Siminairy Zi.**; Fred. No. 88 87; Conservative 57; Mismat	Gaps 16;
; LENGIN: 300 ; TYPE: PRT ; ORGANISM: Homo sapiens ;;15-10-511-037-2505	Qy 2 SESNSTGILPPAAQVPLAFLMSFAFAI-MVGNAVVILAFVVDRNLRHRSNYF	RSNYF 53 ::   STDTF 91
Duery Match 9.9%; Score 203		105
Similarity 21.4%; Pred. No. 1.5e-10; 7; Conservative 57; Mismatches 126;	92	AGALL 141
Qy 2 SESNSTGILPPAAQVPLAFLMSSFAFAI-MVGNAVVILAFVVDRNLRHRSNYF 53 :   : :   : :   : :   : :   : :   : :   Db 32 NESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRTALSSTDTF 91	Qy 106 -VLISYDRYQSVSNAVS-YRAQHTGIMKIVAQMVAVWILAFLVNGP-MILASDSWKNSTN	KNSTN 162   DERLN 199
54 PLNLAISDFLVGLISIPLYIPHVLFNWNFGSGICMFWLITDYLLCTASVYNI	163	AGFST 220
92 LLHLAVADILL-VLILLENAAVDAAVQNVFGSGLCKVAGALFININFIAGALL	200 AIRCQINFEQVEKIALKVLQLVAGFLLFLELLVRAIT————————————————————————————————————	
DY 106 -VLLSTBYRQDSNAYD-IKACHIGIRKIYAQNAYMILAFLNAGF-MILASDSWANDIN 102  Db 142 LACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLFFBLPDFIFLSAHHDERLN 199	Db 239	
163 TKDCEPGFVTEWYLLTITMLLEFLLPVISVAYFNVQIYWSLWKRRALSRCPSHAGFST	281 FWRSESAALRQREYAE	
	246RGQRRLRAMRLVVVVVAFALCWTPYHLN	LGALA 287
221 TSSSASGHLHRAGVACRTSNPGLKESAASRHSESPRRKSSILVSLRTHMNSSITAFKVGS		
DD 239 245		

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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
TITLE OF INVENTION: 641, 260, 55689, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 12303, 986, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: MPIO2-012PIRM OWNI
CURRENT APPLICATION NUMBER: US/11/302,678
CURRENT FILING DATE: 2005-12-14
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PRIOR FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-02-8
PRIOR PILING DATE: 2002-02-8
PRIOR PLING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-09-27
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-11-05
PRIOR PILING DATE: 2002-11-05
PRIOR FILING DATE: 2002-11-05
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PRIOR APPLICATION NUMBER: US 60/349,511
                                                                                                                                                                      APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Venkateswarlu, Karicheti
Sequence 59, Application US/11302678 Publication No. US20060088881A1
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AF307973 Homo sapi
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AF329449 Homo sapi
AF329429 Homo sapi
AK376577 Sequence
AK3701229 Sequence
BD095598 Novel gua
AB045370 Homo sapi
BC112348 Homo sapi
BC112348 Homo sapi
AK549343 Sequence
AF31230 Homo sapi
AF349343 Novel gua
AB04934 Homo sapi
AB097512 Novel gua
AB189711 Macaca fa
AB053300 Sus scrof
AF38858 Cavia por
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AC007922 Homo sapi
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Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation
Unpublished
(bases I to 1538)
Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Direct Submission
Submitted (12 AMAR-2001) Molecular Pharmacology, The R.W. Johnson
Submitted (12 Lamare Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Mus musculus histamine H4 receptor mRNA, complete cds.
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    organism="Mus musculus"
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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TNTBECEPGFVTEWYILAITAFLEFILPVSLVVYFSVQIYWSIWKRGSLSRCPSHAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                         841 ATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGGTTCC
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                                                                             IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer
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                                        ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer
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Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Comparison of human, mouse, rat, and guinea pig
receptor suggests substantial species variation
Unpublished
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Liu,C., Wilson,S., Kuei,C. and Lovenberg,T.W.
Direct Submission
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/db_xref="G1:15420537"
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Rattus norvegicus
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YNIVIISYDRYGNSVANVSYRAQHTGIMKINAQMYAWILAFLWNGPMILASDSWKNS
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BRPKSWWYSIARWLGNWRSFVNRPELYPCHRROGKAFWILLCTTKQPALSQNGSVSS
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                                                              /note="G-protein-coupled receptor"
                                                                                               /product="histamine H4 receptor"
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/db_xref="G1:15420535"
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/IiMI at: http://image.llnl.gov Series: IRAM Plate: 15 Column: 19.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                          /mol_type="mkNA"
/db_xref="taxon:10090"
/clone="MGC:130500 IMAGE:40046148"
/tissue type="PCK rescued clones"
/clone_lib="NIH MGC 285"
/note="Vector: PCR Ealunt II-TOPO with reversed insert;
Clone identification sequence tag: GTGGTTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe
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/gene="Hrh4"
/note="synonyms: H4, H4R, BG26, HH4R, AXOR35, GPRv53,
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Conservative:
Mismatches:
Indels:
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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/codon_start=1
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                                                                                        ValTrplleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLys 158
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                           | IleThrMetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGln
                  AlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAla
                                        93213 TAGGTGTCTTATAGGGCTCAACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCT
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1 (bases 1 to 1173)

1 (bayes,T., Shapiro,D.A., George,S.R., Setola,V., Lee,D.K. Cheng,R., Rauser,L., Lee,S.P., Lynch,K.R., Roth,B.L. and O'Dowd,B.F.
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93300 GCCAACATCACGTGAGTTAGTGTAGCTCTTGCATATCCC-------TGGAAC 93256
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                                                                                                                                                                                                                                                                                                Wilson,R.K.
Direct Submission
Submitted (11-FEB-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Feb 11, 2004 this sequence version replaced gi:38194370.
                                                                                                                                                     Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 199837)
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Submitted (06-NOV-2003) Genome Sequencing Center, 4444
Parkwaty, St. Louis, MO 63108, USA
4 (bases I to 199837)
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Center code: WUGSC
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33
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Matches:
Conservative:
Mismatches:
Indels:
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Contact: submissions@watson.wustl.edu
------- Project Information
Center project name: M_BA0314021
                                                              The sequence of Mus musculus clone
Unpublished
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                                                                                                     2 (bases I to 199837)
McPherson, J.D. and Waterston, R.H.
Direct Submission
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-314021"
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GSECEPGFFSEWYILAITSFLEFVIPVILVAYFUNMIYWSIJKRDHLSRCOSHPGLTA
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/t=anslation="WADTWST1"LSLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDK

NLRHRSSYFFLNLAISDFFVGVISIPLYIPHTLFEWDFGKEICVFWLTTDYLLCTASV
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                                                                                                               Organization (173)

Nguyen, T., George, S.R., Lee, D.K., Cheng, R., Lynch, K.R. and O'Dowd, B.F.

Submitssion
Submitted (26-SEP-2000) Pharmacology, University of Toronto, Taddle Creek Rd., Rm. 4353, Toronto, Ont MSS 1A8, Canada 1.1173
Discovery of a novel member of the histamine receptor family
                                                           and
                                          2 (bases 1 to 1173)
Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R.
O'Dowd,B.F.
                                                                                     Discovery of H4, a Novel Histamine Receptor
Unpublished
                                                                                                                                                                                                                                                                                                                                                         /note="G protein-coupled receptor"
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Mismatches:
Indels:
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/product="histamine receptor H4"
         Mol. Pharmacol. 59 (3), 427-433 (2001) 11179435
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Matches:
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                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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/gene="H4"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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PN JP 2001211889-A/1

PN JP 2001211889-A/1

PD 07-AGG-200

PD 200-200-2000

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PD 2000329359

PR 29-OCT-1999 GB 9925641:4,20-APR-2000 GB 0009973:9 PI

BEAT PETER, MARK ANTONY OLAYLEE

PC AG1P11/00,

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Location/Qualifiers
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Conservative:
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1 (bases 1 to 1173)
Peter, B. and Olaylee, M.A.
Novel polypeptide
Patent: JP 2001211889-A 1 07
PFIZER INC
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JP 2001211889-A/1.
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Homo sapiens
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Novel polypeptide.
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Matches:
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Pred. No.:
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Oy 361 ProLeuCysHishrgArgArgDheGlnLysAlaPheTrpLys11eLeuCysVal	Homo sapiens Eukaryota; Me Mammalia; Eut Hominidae; Ho 1 Othen, R. Human Orphan Parent: EP 15 Arena Pharmac Loca Loca (org	Alignment Scores: 1.19e-132 Length: 1173  Pred. No.: 1370.50 Matches: 267  Score: 1370.50 Conservative: 40  Best Local Similarity: 68.3% Mismatches: 82  Query Match: 2 Gaps: 2  DB: 2 Gaps: 2  US-10-626-445-8 (1-391) x CS173186 (1-1173)  Qy	Db 1 ATGCCAGATACTAATAGCACAATCTATTATCACTAAGCACTCGIGTTACC  Qy 21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIle  Db 21 TTATGTCCTTAGTAGCTTTTGCTATAATGCTATGGTCATT  Qy 1 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu  Db 121 GTGGTGGACAAAACCTTAGAAGATGGTTTTTTTTTTTTT	StandbedlySerGlyIleCysMetPheTrpLeulleThrAspTyrLeuLer
MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 20	AsnPheGlySerGly11eCysMetPheTrpLeulleThrAspTyrLeuLeuCysThrAla 10  :::	421 GrGCTGGCCTTCTTAGTGATGGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGATGAA 480  161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180  181 GGTAGTGAATGTGAACTGGATTTTTTTCGGAATGGTACATCCTTGCCATCACA 534  181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200  182 TCATTCTTGGAATTCGTGATCCTCAGTCATCTTAGTCGTTTTTTTT	ThrserserslaserdlyHisLeuHisArgAladlyValAlaCysArgThrserAsn	281 PheTrpArgGerGluSerAlaAlaLeuArgGluTyrAlaGluLeuLeuArgGly 300 835 TTCTCCAATCAGTTCTGACTTCTCCACAAGGGACATGTGAACTGCTTAGAGCC 894 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaFro 320 895 AcGAGATTAGCCATCTCTTAGGGGTTTTTGCTGTTTGCTGGGCTCCA 954 321 TyrCysLeuPheThxIleValLeuSerThxTyrProArgThrGluArgProLysSerVal 340 826 TATTCTCTGTTCACAGTCCTTTAGTTTTATTCTGTTTTGCTGGGCTCCA 954 827 TyrCysLeuPheThxIleValLeuSerThxTyrProArgThrGluArgProLysSerVal 340 837 TyrCysLeuPheThxIleValLeuSerThxTyrProArgThrGluArgProLysSerVal 340 838 TyrCycSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 839 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 831 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 832 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 833 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 834 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 360 835 TyrTyrSerIleAlaPheTrpLeuGlnTxpPheAsnSerPheValAsnProPheLeuTyr 370

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LeuCysThrala 100
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|TTATGTACAGCA 300
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Alignment Scores:    1.196-132   Langth: 1173   Scores: 1170   Sco	241 ProGlyLeuLygGluSerAlaAlaSerArgHisSerGluSerProArgArgLySerSer 715 TCTGCATCGACAGAAGTTCCTGCATCTTCATCCAGAGACAGAGAAGAGTAGT 261 IlleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 175 CTCATGTTTTCCTCAAGAACGATGAATAGCAATACAATA
161 ThrAsmThriyaAspCysGlubroGlyPheValThrGluTrpTyrIlleLeuThrIlleThr 180 481 GGTAGT	New Control   New Control

RESULT 9
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                                                                                                    201 TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr
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                                                                                                                                               221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn
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Umland,S. and Wang,S.
Histamine receptor
Patent: WO 0125432-A 1 12-APR-2001;
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                                                        341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
                                                                                                   361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
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            TyrCysLeuPheThr11eValLeuSerThrTyrProArgThrGluArgProLysSerVal
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Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Umland,S.P. and Wang,S.
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Matches:
Conservative:
Mismatches:
Indels:
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Patent: US 66133334 Renliworth, NJ
Schering Corporation; Kenliworth, NJ
Location/Qualifiers
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    11.1173
    organism="unknown"
    /mol_type="genomic DNA"

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Unclassified.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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            PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly
                         TTCTCCCAATCAGATTCTGTAGCTCTTCACCAAAGGGAACATGTTGAACTGCTTAGAGCC
                                                                            TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal
                                                                                                                               TATTCTCTGTTCACAATTGTCCTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT
                                                              ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro
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G-protein coupled receptor-like polypeptide
Patent: EP 1096009-A 1 02-MAY-2001;
Pfizer Limited (GB); PFIZER INC. (US)
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Sequence 1 from Patent EP1096009.
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AX139113.1 GI:14274791
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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            Location/Qualifiers
CORPORATION (US)
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181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTCGAATGG
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DEFINITION ACCESSION VERSION KEYWORDS

AX301763

LOCUS

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IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                          Jones, P.G., Blatcher, M., Wu, S. and Pausch, M.H. Human histamine h 47 receptor Patent: WO 185786-4 115-NOV-2001; American Home Products Corporation (US) Location/Qualifiers
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Mismatches:
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                        GTCTCCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT
                               241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer
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                                                                                                 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer
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Jones, P.G., Wu,S. and Betty, M.
Jones, P.G., Wu,S. and Betty, M.
Submitssion
Submitted (25-SEP-2000) Neuroscience, Wyeth Ayerst, CN8000,
Princeton, NJ 08543, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCTACCATCACAACACAGTCGGTCAGTATCTTCT 1170
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/note="G protein coupled receptor"
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Jones, P.G., Wu,S. and Betty, M.
Cloning of a novel histamine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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LOCUS

EATURES

rcent Sim st Local ery Match : :-10-626-4	41 41 121	Oy 61 AB Db 181 GA Qy 81 AS Db 241 GA	301	Oy 121 Se Db 361 TC Oy 141 11 Db 421 GT	Qy 161 Th Db 481 GG Qy 181 Me	Db 535 TC Qy 201 Tx Db 595 TG	Qy 221 Th Db 655 GT Qy 241 Pt	Db 715 TC Qy 261 11 O C C C C C C C C C C C C C C C C C	
301 ArglysLeuhlaArgSerLeuhlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320 895 AGGAGATTAGCCAAGTCACTGGCCATTCTTAGGGGTTTTTGCTGTTTGCTGGGCTCCA 954 321 TycCysLeupheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340 11 C	361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380	AF325356 1173 bp mRNA linear PRI 11-SEP-2001 Homo sapiens histamine receptor H4 (AXOR35) mRNA, complete cds. AF325356 AF325356.1 GI:15553202		Hominidae; Homo I (bases 1 to 1173) Zhu,Y., Michalovich,D., Wu,HL., Tan,K.B., Dytko,G.M., Mannan,I.J., Boyce,R., Alston,J., Tierney,L.A., Li,X., Herrity,N.C., Vawter,L., Sarau,H.M., Ames,R.S., Davenport,C.M., Hieble,P., Wilson,S., Bergsma,D.J. and Fitzgerald,L.R. Cloning, expression, and pharmacological characterization of a	ri	Submitted 1539, King 1	/db_xref="taxon:9606" /chromosome="18" /map="18q11.2" 1. 1173 /gene="AXOR35" 1. 1173	/gene="AXOR35" /codon_start=1 /product="histeamine_receptor_H4" /protein_id="AAL01684.1" /db_xref="G1:15553203" /translation="MPDTNSTINESLSTRVTLAFFMSLVAFAIMLGNALVILAFVVDK NLRHRSSYFFLNIA.1SDFYGV1S1PLY.IPHTLFRWDFGKEICVFWLTTDYLLCTASV NNIVLISYDRYLSVORNAVSYRTQHTGVLKIVYTLWYAWWLAFLVNGPMILVSESWKDE GSBECBREPSBRYTILAITSFLERFYIPVILVAYFRNMIYWSLWKRHSHSRCQFHFGLIAA vscnifflerperisspenger, saperpalasherpengerstanderingspengers	GSFSQSDSVALHQREHVELLRARRLAKSLÄJLLGVFAVCWAPYSLFTIVLSFYSSATG PKSVWYRIAFWLQWFNSFVNPLLYPLCHKRFQKAFLKIFCIKKQPLPSQHSRSVSS"
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	2	RESULT 15 AF325356 LOCUS DEFINITION ACCESSION VERSION	KEIWOKUS SOURCE ORGANISM	REFERENCE AUTHORS TITIE	JOURNAL PUBMED REFERENCE AUTHORS TITLE	JOURNAL FEATURES SOUTCE	gene		ORIGIN

Length: Matches:

Alignment Scores: Pred. No.:

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TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
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Adgg 8755 Human Orp
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Adj 2632 Human CDN
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Adg 20167 Human G p
Ady 8839 Human Dis
Adv 43700 Human Dis
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Ab478739 Nucleotid
Aai7750 Human his
Aai67750 Human his
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                          nucleic search, using frame_plus_p2n model
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Database

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Result Š.

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The present sequence is that of a cDNA clone encoding a murine histamine receptor of the H4 subtype. The CDNA was isolated from a mouse spleen con A library. It shows 72.8 homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the mammalian histamine H4 receptor. Such modulators may be used in gene therapy as that all and activity cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity
                                                                                                New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.
                                                                                                                                                                                                                 Claim 4; Fig 5A; 92pp; English
                         WPI; 2002-114339/15
                                                  P-PSDB; AAM50565
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Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;

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Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similari DB:	tent Scores: No.: t Similarity cocal Similar Match:	res: arity: milarity:	2.1e-171 2035.00 99.7% 99.7% 69.4%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1176 390 0 0 0
US-10-626-44	5-445-1	-8 (1-391)	x AAI70981 (1.	-1176)	
δλ	н	MetSerGlu	SerAsnSerThrGly	MetSerGluSerAsnSerThrGly11eLeuProProAlaAlaGl	AlaGlnValProLeuAlaPhe 20
qq	н	ATGTCGGAG	ATGTCGGAGTCTAACAGTACTGGCAT	CATCTTGCCACCAGCTG	CTTGCCACCAGCTCCCCTTGGCATTT 60
٥٨	21		SerPheAlaPheAl	LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValIl	AlavalvalileLeuAlaPhe 40
οp	61	TTAATGTCT	TCATTGCCTTTGC	TATAATGGTAGGCAATG	TTAATGCTTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCTTTAGCCTTT 120
λ̈́o	41		ValValAspArgAsnLeuArgHisArgSerAsnTy	SArgSerAsnTyrPheE	rPhePheLeuAsnLeuAlalleSer 60
ΩÞ	121	GTGGTGGAC	AGAAACCTTAGACA	rcgaagtaattattrt	GIGGIGGACAGAAACCTTAGACATCGAAGTAATTATTTTTTTTTT
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qq	181	-	GTGGGTTTGATTTC	GACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCC	ccrcacgrdrrrraacrdg 240
'n	81		SerGlyIleCysMe	AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspI	AspTyrLeuLeuCysThrAla 100
ОР	241	-	AGTGGAATCTGCAT	GTTTTGGCTCATTACTC	AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA 300
λō	101	ServalTy	rAsnIleValLeuIl	SerTyrAspArgTy	rGlnSerValSerAsnAlaVal 120
đ	301		AATATTGTCCTCAT	TAGCTACGATCGATACC	TCTGTCTACAATATTGTCCTCATTAGCTACGATCGATACCAGTTTCAAATGCTGTG 360
ò	121	ω –	AlaGlnHisThrGl	VIleMetLysileValA	erTyrargAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140
qq	361		GCTCAACACACTGG	CATCATGAAGATTGTTC	TCTIAIAGGGCTCAACACACACTGGCATCAIGAAGAITGTIGCICAAAIGGIGGCIGITIGG 420
٥٨	141		PheLeuValAsnGl	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaS	SerAspSerTrpLysAsnSer 160
qa	421		TTCTTGGTAAATGG	CCCGATGATTCTGGCT	ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGATTCTTGGAAGAACAGC 480
ò,	161	ThrAsnThrI	ysaspcy	sGluProGlyPheValThrGluTrp 	TrpTyrileLeuThrileThr

Mus musculus

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961 TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG 1020
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481 ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCATTACA 540
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                                                                181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr
                                                                                                                         TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr
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Li F; eng H;

Hohmann J,

JE, Gragerov A, Hohmann J, Pavlova MN, Vassilatis D,

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Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
                                                                                                                                            Claim 151; SEQ ID NO 1360; 542pp; English.
                                                                                                                                 pectoris, Parkinson's disease.
                              09-SEP-2003; 2003WO-US028226.
                                          09-SEP-2002; 2002US-0409303P.
                                                                         AA, Bergmann JE,
Mcilwain KL, Pa
                                                                                            WPI; 2004-390329/36.
                                                             (PRIM-) PRIMAL INC.
                                                                                                  P-PSDB; ADO29497.
                                                                         Gaitanaris GA,
                   13-MAY-2004
                                                                               Madisen L,
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The invention relates to human and mouse G protein-coupled receptors (GPCRS) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, proventing or diagnosing diseases of section of the invention; methods of sectioning diseases as a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a GPCR gene of the invention; and with capture of the transgenic mouse comprising and expression mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention and kits comprising probes which hybridise to GPCR polyuncleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, disease, disarchoen, disease or schizophrenia); disorders of the adrenal gland, disorders of the colon or intestine syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders (e.g., autoimmune disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid carthials gout or osteoporosis); method diseases or vitamin deficiency-related diseases or vitamin deficiency-related diseases or vitamin disorders or thereis, ship prostate, testine, ship proteins such proteins seminar seminar seminar seminar seminar seminary seminary such cardials. The protein seminary uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Other; Sequence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0

	1538	390	0	1	0	0	
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	(1-1538)
	3.07e-171	2035.00	99.78	99.78	99.48	12	x AD030257
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	US-10-626-445-8 (1-391) x ADO30257 (1-1538)

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1020 TACTGTCTGTTCACAATTGTCCTTTCAACTTACCCCAGAACGGAACGCCCCAAATCGGTG 1080 TGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTTAATCCCTTTCTGTAC 1140 CCTTTGTGTCACAGGCGTTTCCAGAAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1200 100 180 300 360 420 140 480 160 540 180 9 200 9 720 240 780 280 900 300 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAanSerPheValAsnProPheLeuTyr 360 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380 ArglysteuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340 80 40 9 ThrasnThrLysAspCysGluProGlyPheValThrGluTrpTyrlleLeuThrlleThr AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA GACTICCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCACGGGTTGTTTAACTGG AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp ACCTCTTCCAGTGCTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer ATCCTGGTGTCCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAGTGGGTTCC TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 121 TTAATGTCTTCATTTGCCTTTGCTATAATGGTAGGCAATGCTGTGGTCATCTTAGCCTTT ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaileSer AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTGG IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTGGCTTCAGATTCTTGGAAGAACAGC 541 ACGAACACAAAGGACTGTGAGCCTGGCTTTTGTTACAGAGTGGTACATCCTCACCATTACA MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr regadecercidedaadeceradegecrercagradereceradeceargerecaer ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn ccregarreaaggaarcagcrecregreacrecreagaaagrecregaagaagaagcage IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391 181 1021 341 1081 1141 41 61 241 81 301 101 361 121 421 141 481 161 601 661 721 241 781 261 841 281 901 301 961 181 201 221 321 361 d 8 셤 ò 요 ò ద ठे g 8 8 8 8 y 8 8 6 8 6 g ò 8 & 중 음 ò g ò ద à g ઠ g à us-10-626-445-8.p2n.rng

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modulators of the mammalian histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of a cDNA clone encoding a rat histamine receptor of the H4 subtype. The CDNA was isolated from a rat spleen cDNA library. It shows 72.5% homology to the human H4 receptor coding region. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAB50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                           Histamine H4 receptor; rat; antiasthmatic; antiallergenic; antinflammatory; cardiant; circulatory; antidiabetic; laxative; diagnosis; gene therapy; ss.
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1201 CCAGCGCTGTCACAGAACCAGTCAGTATCTTCT 1233
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                                                                                                                                                                                                                                                                                                                                      Rat histamine H4 receptor cDNA
                                                                                                                                                   AAI70982 standard; cDNA; 1176
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Length:
Matches:
Conservative:
Mismatches:

1.47e-145 1745.00 89.3% 84.9% 85.2%

Best Local Similarity:

Query Match: DB:

Percent Similarity:

Indels: Gaps: (1-1176)

US-10-626-445-8 (1-391) x AAI70982

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel splice variants of human H4 histamine receptor, H4b and H4c, useful for identifying agonists or antagonists of the receptor which are useful for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.
                                                                                                                                                                                     Human; H4; histamine receptor; inflammatory bowel disease; psoriasis; atopic dermatitis; stroke; myocardial infarction; migraine; allergy; chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy; rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to splice variants of human H4 histamine receptor, H4b and H4c. The invention is useful for identifying an agonist, antagonist or inverse agonist of a mammalian histamine receptor. The agonist, antagonist or inverse agonist of H4b and H4c is useful for treating inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, or psoriasis. The present sequence is human H4 receptor DNA
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267
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/note= "CDS does not include stop
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Matches:
Conservative:
Mismatches:
Indels:
Disclosure; Page 56-58; 31pp; English.
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                          Human H4 receptor wild-type DNA
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1370.50
78.3%
68.1%
66.9%
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13-NOV-2001; 2001US-0332697P.
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                                                                                                                                                                                                                                                 asthma; receptor; gene; ds
                                                                                                                               (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallagher MJ, Yates
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MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe

x AAD55126 (1-1170)

JS-10-626-445-8 (1-391)

Similarity:

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Query Match: DB:

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The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB602855 to AAB602859 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                 Human, G protein coupled receptor; GPCR; transmembrane receptor;
identification; agonist; screening; therapeutic; pharmaceutical; mutant;
                                                                                                                                                                                                                                                                                       Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13
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Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists.
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                                                                                                                                                                                                                                                                                 G procein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned by RT-PCR using human peripheral leucocyte cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane alpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal
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                                                                                                                                             321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340
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              IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer
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transmembrane receptor; signal cascade; ss.
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141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
                                                                                                                                                 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GPCR)-like polypeptide, designated PPI-013. The PPI-013 protein can be expressed by standard recombinant methodology. Antibodies and modulators of PPI-013 are useful in the manufacture of a medicament for treating allergic disorder, including extrinsic asthma, immunological disorders, such as intrinsic asthma, vasculitic granulomatous disease, interstitial and other pulmonary disease, including chronic obstructive pulmonary disease (COPD), infectious, inflammatory disease, such as inflammatory bowel disease and neoplastic and myeloproliferative diseases.
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ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT
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PFIZ ) PFIZER INC.
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Location/Qualifiers 1. .1173

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/\*tag=

Human G protein-coupled receptor AXOR35 cDNA.

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AsnPheGlySerGlyIleCysMetPheTrpLeulleThrAspTyrLeuLeuCysThrAla 100
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(first entry)

10-AUG-2001

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The invention relates to the human G protein-coupled receptor AXOR35 and variants. Like all G protein-coupled receptors, AXOR35 fragments and variants. Like all G protein-coupled receptors, AXOR35 fragments are divisionally and structural similarity with G protein-coupled receptors Buch be homeology and structural similarity with G protein-coupled receptors Buch captession of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins and nucleotides may be used to treat a wide variety of disorders including bacterial, fungal, protezal and viral infections, particularly HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy; calabetes; obesity; anorexia; bulmia; osteoporosis; sathma; allergies; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting; psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retained of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes of strokes and severe mental capters of strokes and severe strokes and severe mental capters of strokes and severe strokes and severe mental capters of strokes and severe strokes and severe mental capters and severe strokes and severe strokes and severe severed severed severed severed severed severed severed severed severed severed severed severed severed severed severed severed severed severed severed severed severed severed severed severed seve
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                                                                               histamine H3 receptor homologue, infection, viral, bacterial, fungal, protozoan, HIV-1; HIV-2; pain, cancer; diabetes, obesity, anorexia, bulimia, osteoporosis, asthma, allergy, urinary retention, acute heart failure, hypotension, allergy, urinary retention, myocardial infarction; stroke; ulcer; migraine; vomiting, myocardial infarction; stroke; ulcer; migraine; vomiting, psychotic discorder; neurological disorder; anxiety; schizophrenia; manic depression; bipolar disorder; parkinson's disease; Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte; macrophage; eosinophil; neutrophil; function modulation; autoimmune disorder; pulmonary disorder; gene therapy; vaccine; drug screening; signal transduction; transgenic animal; drug discovery;
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                                                             AXOR35; human; G protein-coupled receptor; 7TM receptor;
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/note= "G protein-coupled receptor"
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Michalovich D, Morrow DM, Zhu Y;
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03-FEB-2000; 2000US-00497790.
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P-PSDB; AAB73622.
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disease via the detection of abnormal levels of protein or mRNA, or via disease via the detection of abnormal levels of protein or mRNA, or via althe detection of mutations in the corresponding gene. AXOR35 proteins are also useful for inducing an immunological response in a mammal against the above diseases, and for antibody production. AXOR35 nucleotides are also useful as diagnostic reagents, in chromosome localisation and tissue expression studies, and for producting transgenic animals useful in drug discovery. AXOR35-specific antibodies are useful for purifying the AXOR35 associated with the expression of the AXOR35 protein or fragments thereof, and are also useful for treating conditions sequence represents cDNA encoding human AXOR35 protein. The present
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                                                                                 281 PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly 300
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                                                                                                                                                                                          TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal
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                                                                                                                                                       This sequence represents the open reading frame for a human histamine receptor (HR) designated SP9144. The sequence was isolated by searching databases with the sequence of known G-coupled protein receptor (GCPR). The gene is used for recombinant production of HR and for preparing antibodies (Ab). These Ab are used to purify HR by immunoaffinity clowantibodies (Ab). These Ab are used to purify HR by immunoaffinity clower that express the receptor, as antagonist to block binding of histamine (for treating any histamine-associated disorder) and to generate anti-idiotypic antibodies. Agonists and antagonists of the HR protein can be used in the treatment of e.g. inflammation, asthma, allergy, atopic dermatitis, stroke, myocardial infarction, migraine, chronic obstructive pulmonary disease, rheumatoid arthritis, multiple
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      antibodies, e.g. for treating-histamine related
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                                                                                                                                                                                                                                                                                   The present sequence encodes a human histamine receptor. The polypeptide is useful for identifying an agonist or antagonist of a mammalian of listamine receptor. It is useful as an antigen to elicit the production of antibodies. The histamine receptor polypeptide and polymuclectide are useful in the treatment and management of diseases such as inflammation, asthma, allergy, atopic dermatitis, strok, myocardial infection, migraine, chronic obstructive pulmonary disease (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel disease and psoriasis. They are also useful for modulating intracellular second messenger pathway activated through histamine receptors (cyclic-AMP, calcium, inositol phosphate and mitogen activated protein (MAP) kinase), changes in cellular growth rate, secretion of hormones, receptor-stimulated Ca2+
                                                                                                                                                                                   Novel mammalian histamine receptor polypeptide useful for identifying agonist or antagonist for treating diseases such as inflammation, asthma, stroke, migraine, rheumatoid arthritis, multiple sclerosis, psoriasis.
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1 ATGCCAGATACTAATAGCACAATCAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT
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MONSMA F J.
MORSE K L.
UMLAND S P.
                                                                                                                                     2002-673827/72.
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Best Local Similarity:
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121 GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGATGAA 480
                                                                                                                                                                                                                         535 TCATTCTTGGAATTCGTGATCCCAGTCATAGTCGCTTATTTCAACATGAATATTTAT 594
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                                                                                                                481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCCATCACA
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                                                                                                                                                             The present sequence is that of cDNA clone pH4R encoding a human histamine receptor of the H4 subtype. The cDNA was isolated from a bone marrow cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAT70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the human histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allerange may be useful for diagnosing, treating or preventing asthma, insulin dependent diabetes mellitus, hyperglycemia, constipation, insulin dependent diabetes mellitus, hyperglycemia, constipation, arxhythmia, disorders of the neuroendocrine system, stress and spasticity
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                                                                                          New mammalian histamine H4 receptor proteins and polynucleotides enc
the proteins, useful in gene therapy for treating diseases where it
beneficial to elevate mammalian histamine H4 receptor activity.
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            (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                           Claim 4; Fig 1; 92pp; English.
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                                      GGTAGT------GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCCATCACA
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The invention provides an isolated histamine receptor, H4, which binds ligands comprising imidazole attached to amine by an alkyl chain. The H4 receptor can be expressed by standard recombinant methodology. Cells expressing H4 receptor protein at a detectable level can suppress cyclic adenosine monophosphare (cAMP) formation when contacted with the H4 receptor agonist. The H4 receptor and antibodies are used for identifying H4 receptor modulators. Modulation of histamine H4 receptors is useful for treating transplanted organ rejection, asthma, allergies and autoimmune pathologies such as multiple sclerosis, type I diabetes, protein and nucleic acids are useful targets to identify drugs that are effective in treating disorders associated with histamine-regulated processes. Identification and isolation of H4 receptor provides for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             development of screening of molecules that interact with H4 receptors. Genetic variants of H4 can be used to diagnose an H4 associated disease as described above. The H4 receptor polynucleotide is useful to treat or prevent a disorder associated with the function of H4 in peripheral blood
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                                                                                                                                                                                                                                                                        New histamine receptor, termed H4 useful for detecting H4 (ant)agonists for treating transplanted organ rejection, asthma, allergy, multiple sclerosis and rheumatoid arthritis.
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                                                                                                                                       (AMHP ) AMERICAN HOME PROD CORP
                                                                                                                                                                                                                                                                                                                                                              Claim 13; Fig 1; 66pp; English
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                                                                           23-AUG-2000; 2000US-0227567P. 13-NOV-2000; 2000US-0247855P.
                    04-MAY-2001; 2001WO-US014527.
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                                                                                                                                                                                                                      WPI; 2002-049442/06.
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1075 CCATTGTGTCACAAGCGCTTTCAAAAGGCTTTCTTGAAAATATTTTGTATAAAAAGCAA 1134
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hARE-5; hRUP3; hRUP5; hRUP7; hGPCRZ7; hARE-1; hARE-2; hPPR1; hG2A;
hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUF4; signalling cascade.
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301 rergrararararistecreareacerateareareareareareareareareare
                                              141 IleLeuAlaPheLeuValAsnGlyProMetileLeuAlaSerAspSerTrpLysAsnSer
                                                                                                            181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr
                                                                                                                                                                                                                                   655 GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT
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                            SerTyrArgAlaGlnHisThrGlylleMetLysIleValAlaGlnMetValAlaValTrp
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LeumetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe

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ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer

AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal TCTGTATATAAACATTGTCCTCATCAGCTATGATCGATACCTGTCAGTCTCAAATGCTGTG

81

241 101 301 121 361 141 421 161

AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp

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240 100 300 120 360 140 420 160 480 180

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The invention relates to a human G protein-coupled receptor (GPCR)
appearing as ABU92259-ABU92277 (encoded by CDNAs ACA93256-ACA93274) named
hare-3, hARE-4, hARE-5, hRUPS, hRUPS, hRUPS, hRUPS, hROFRZT, hARE-1, hARE
-2, hPPR1, hG2A, hCHN3, hCHN4, hCHN6, hCHN8, hCHN9, hCHN10 and hRUP4.
Also included are a plasmid comprising a vector and one of the CDNAs
chove and a host cell comprising the plasmid. The GPCRs are useful for
the direct identification of candidate compounds as inverse agonists,
agonists or partial agonists. In vitro and in vivo systems incorporating
GPCRs is useful for elucidating and understanding the roles these
creceptors play in the human condition, both normal and diseased, as well
as understanding the signalling cascade. The CDNAs are useful for making a
understanding the signalling cascade. The CDNAs are useful for making a
dientification of the expression of the receptor in tissue samples. The
present sequence is a CDNA encoding a GPCR of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel endogenous, orphan, human G protein-coupled receptors useful identification of modulators of the receptor and as research tools understanding the role of the receptor in human body.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen R, Dang HT, Liaw CW, Lin I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; Page 22; 54pp; English
                                                                                                             980S-0109213P.
990S-0121845P.
990S-0123946P.
990S-01239449P.
990S-0136437P.
990S-0136437P.
990S-0136437P.
990S-013121P.
990S-0137127P.
990S-0137121P.
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990S-0156555P.
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LIAW C V
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28-MAY-1999;
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200 594 220 654

TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr

ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn

8 6 8 6

Grerérrecaacarergadacacrearreagageragacrarerreaggagererr 241 ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 

TCATICITGGAATICGTGATCCCAGTCATCTTAGTCGCTTATTTCAACATGAATATITAT

181 535 201 595 221 655

8 6 8 6

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SerTyrArgAlaGlnHisThrGly1leMetLys1leValAlaGlnMetValAlaValTrp

IleLeuhlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer  ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrlleLeuThrlleThr

481 GGTAGT-----GAATGTGAACCTGGATTTTTTCGGAATGGTACATCCTTGCCATCACA MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 260

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        261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer
                                                PheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArgGly
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MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe 

1173 267 40 82 3

Length: Matches: Conservative: Mismatches: Indels:

3.49e-112 1370.50 78.3% 68.1% 66.9%

Best Local Similarity:

Query Match: DB:

Percent Similarity:

Alignment Scores: Pred. No.: Score:

Gaps:

US-10-626-445-8 (1-391) x ACA93262 (1-1173)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides novel human G protein-coupled receptor (GPCR) proteins and their encoding nucleic acids. The invention is useful for making a probe for dor-blot analysis and for RT-PCR identification of the expression of the receptor in tissue samples. The invention is also useful for identifying candidate compounds as inverse agonists, agonists or partial agonists and as research tools in determining the location of the receptors within the body. The present sequence is human orphan G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cDNA encoding a human G protein coupled receptor, useful for making probe for dot-blot analysis against tissue-mRNA, and/or for RT-PCR identification of the expression of the receptor in tissue samples.
                                                                                                                       Human; G protein-coupled receptor; GPCR; research tool; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
CCTCTACCATCACAACACAGTCGGTCAGTATCTTCT 1170
                                                                                                                                                                                    /product= "Human GPCR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 13; 52pp; English
                                                                                                                                                       Location/Qualifiers
1. .1173
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99US-0120416P.
99US-0121852P.
99US-0123946P.
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99US-0136439P.
99US-0136567P.
                                               ADG98759 standard; cDNA; 1173
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                                                                                                    Human orphan GPCR cDNA, RUP7
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DANG H T.
LIAW C W.
LIN I.
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28-MAY-1999;
28-MAY-1999;
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12-MAR-1999;
28-MAY-1999;
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Alignment Scores:

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                                                                                                   955 TATTCTCTGTTCACAATTGTCCTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
                                              360
                                                                                                                                                                                                                                                                                                          macrophage; eosinophil; neutrophil; infection; transplant rejection; gastrointestinal disorder; gastric ulcer; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome, vomiting; inflammation; atopic dermatitis; allergy; autoimmume disorder; rheumatoid arthritis; psoriasis; urological disease; urinary retention; cardiovascular disease; myocardial infarction; hypotension; hypertension; pulmonary disorder; renal ischaemia; arteriosclerosis; atheroough; renal disease; renal ischaemia; arteriosclerosis; atheroough; renal disorder; dyskinesia; parkingon's disease; cancer; obesity; stroke; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infections, gastrointestinal disorders, autoimmune disorders, urological diseases, cardiovascular diseases and cancer.
                                                                                         ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated G-protein coupled receptor polypeptide, AXOR35, (and its homologues and variants) and its encoding
TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal
                                           TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr
                                                                                                                                                                                                                                                                                                gene; G-protein coupled receptor; AXOR35; lymphocyte;
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                                                                                                                                                                                                                                                                          Human cDNA encoding G-protein coupled receptor AXOR35.
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                                                                                                                                                CTCTACCATCACAACACAGTCGGTCAGTATCTTCT 1170
                                                                                                                                     ProAlaLeuSerGln -- - AsnGlnSerValSerSer 391
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1, Zhu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/*tag= a
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2000US-00497790.
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Michalovich D, Morrow DM,
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polynucleotide (and its homologues, variants, complements and RNA equivalents). Also included are an anti-AXOR35 antibody, an AXOR35 expression vector, producing a recombinant host cell by introducing the vector into a cell such that the host cell broduces AXOR35, a membrane of the host cell expressing AXOR35, identifying/screening for agonists or antagonists of AXOR35 and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue, by administering to the patient AXOR35 agonists or antagonists. The agonist or antagonist identified is useful for treating a disease such as atthma, or for inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue such as an asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays, for identifying compounds that are agonists or antagonists of AXOR35, as increased the area of a such as a continuous compounds that are agonists or antagonists of AXOR35, as increased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
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IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160 GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGGAAGGATGAA 480 161 ThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThr 180

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341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
                                                                                                                                                                                                                                                                301 ArglysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCCATCACA 534
                             181 MetLeuLeuGluPheLeuLeuProVall1eSerValAlaTyrPheAsnValGlnIleTyr 200
                                        535 TCATTCTTGGAATTCGTGATCCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
                                                                     201 TrpSerieuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
                                                                                  221 ThrSerSerSlaAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
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DW882260 EST 8881
DW306992 DA306992
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DW376242 EST 8881
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BXFZp781C0629_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
DXFZp781C0629_5', mRNA sequence.
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email S. Wiemann@dKfz- heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 81 sequence available.
This clone (DKFZp781C0629) is available at the RZPD in Berlin.
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1 (Dasses 1 to 839)

Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S. EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.) Unpublished (2003)

Contact: MIPS
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AUTHORS
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 BX643713 DKFZp781C
CF147821 AGENCOURT
AK140374 Mus muscu
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  5345.833 Million cell updates/sec
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               GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                           OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                          48236798 seqs, 27959665780 residues
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                                                       25, 2006, 13:51:33
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655... 1111... 113...

Database :

Score

80. Result

857 850 700.5 482.5

EST 25-JUL-2003

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/clone lib="NHH MGC 145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NH-MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: GPCR Consortium cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                    National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                               CF147821
AGENCOURT 14740195 NIH MGC_145 Homo sapiens cDNA clone IMAGE:6971900 5', mRNA sequence.
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RM10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
                                           809 TCTGCATCGACAGAGTTCCTGCATCC 835
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
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    241 ProGlyLeuLysGluSerAlaAlaSer
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1 (bases 1 to 704)
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                                                                                 /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
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/dev_stage="adult"
/lab_host="DH108"
/clone lib="791 (synonym: hlcc4)"
/note="wetvar: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB; cDNA-collection"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 ATGCCAGATACTAATAGCACAATCAATTATCACTAAGCACTCGTGTTACTTTTAGCATTT 155
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1 MetSerGluSerAsnSerThrGlyIleLeuProProAlaAlaGlnValProLeuAlaPhe
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931 AACATCCAGAGGCGCACTCGTCTTCGGCTGGATGGGGGCCGAGAGGCTGGTCCAGAACCC 990
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/protein_id="BAE24362.1"
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                              /clone="B530005H20"
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Futaki, S., Gariboldi, M.,
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Please visit our web site for further details.
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CWGCWPKGHGEAMPLHRYGVGEAGPGVFTGEAGLGGGSGGGAAASPTSSSGSSKTE
RPRSLKRGSKPSASSALEKRWKWYSQSITQRIKLSRDKKVAKSLAIIVSIFGLCWA
YTLLMIIRAACHGHCVPDYWYETSFWLLWANSAVNPVLYPLCHYSFRRAFTKLLCPQK
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 AsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThrMet 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  811 cccgaggccacracracraggrafrcrrcracaacragracrrrcracaggccrcc 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 SerileProLeuTyrileProHisValLeuPhe---AsnTrpAsnPheGlySerGlyIle 86
                                                                                                                                            /note="unnamed protein product; histamine receptor H 3 (MGD|MGI:2139279 GB|NM_133849, evidence: BLASTN, 99%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 LeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 ThrGlylleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 HisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 AlaileMetValGlyAsnAlaValValIleLeuAlaPheValValAspArgAsnLeuArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
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Qy         210	Qy         262 LeuvalSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPhe 281	Qy       322 CysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerValTrp 341         Db       1384 ACACTCCTCATGATCATCGGGTGCTTGCCATGGCCACTGCGTCCCGACTACTGG 1440         Qy       342 TyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyrPro 361         Db       1441 TACGAGACGTCTTCTGGGCCACTCGGCCGTCCTTCACCCA 1500         Qy       362 LeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLys 379         Db       1501 CTGTGCACTACTGGAGCTTCCGTAGAGCTTCTCACAGAGGTCCTTTCACAGAGGTCCTTCACACAGAGGTCCTTCACACAAGAGCTCCTTCACACAAGAGCTCCTTCACACAAGAGCTCCTTCACACAAGAGTCCTTCACACAAGAGCTCCTTCACACAAGAGTCCTTCACACAAGAGCTCCTTCACACAAGAGTCCTTCACACAACAAGAGCTCCTTCACACAAGAGCTCCTTCACACAAGAGTCCTTCACACAACAACAACAACAACAACAACAACAACAAC	RESULT 4  CF147822 LOCUS LOCUS AGENCOURT 14740187 NIH MGC 145 Homo sapiens CDNA clone IMAGE: 6971899 5', mRNA sequence. ACCESSION CF147822 ACCESSION CF147822 ACTIVE REYNORDS SOURCE ORGANISM Homo sapiens CRAYORDS Homo sapiens CRAYORDS Homo sapiens CRAYORDS Homo sapiens CRAYORDS Homo sapiens CRAYORDS SOURCE ORGANISM Homo sapiens CRAYORDS Homo sapiens CRAYORDS Homo sapiens CRAYORDS AUTHORS Homidae: Homo. Hominidae: Homo. Homo	National Cancer Institute / Nith Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: GPCR Consortium CDNA Library Preparation: GPCR Consortium CDNA Library Arrayed by: The I.M.A.G.E. Consortium CDNA Library Arrayed by: The I.M.A.G.E. Consortium Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: IRBIO2 row: b column: 06 High quality sequence stop: 610. FEATURES Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                       DA728518
DA728518 NT2RM2 Homo sapiens cDNA clone NT2RM2001941 5', mRNA
                   81 AsnPheGlySerGly1leCysMetPheTrpLeulleThrAspTyrLeuLeuCysThrAla 100
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                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 IleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPhe 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department o
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
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Mismatches:
                                                                                                                                                                                                      121 SerTyrArgAlaGlnHisThrGlyIleMetLys 131
                                                                                                                                                                                                                                                 382 TCTTATGGAACGCAAAAACGGGGGCCTGAAG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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DA728518.1 GI:81799719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.18e-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456.50
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                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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AUTHORS
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DA728518
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KEYWORDS
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the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pcDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.lani.gov.image.rearrayed_plates/IRBF.preSV.dat
a. Note: this is a NIH_MGC Library."
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Contect: Daniels 8. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute A NIH
Bldg. 31 RmloAD Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTCGAATGG 261
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                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 721)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Matches:
Conservative:
Mismatches:
Indels:
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High quality sequence stop: 328.
Location/Qualiflers
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480.00
83.2%
                                                                                        Homo sapiens (human)
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KEYWORDS
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Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishi, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otuka, R., Yada, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Pujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                             Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xxef="taxon:9606"
/clone="RHHIP2025783"
/clone="type="hippocampus"
/clone lib="BHHIP2"
/note="Vector: pME185FL3"
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                                                                                                                                                                                                                                                                                                                           138 AlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrp 157
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
412 ACCTTCTTTAACCTCAGCATCTACCTGAACATCCAGAGGGGGC-----ACCCGCCT-
                                                                ---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 GluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSerVal
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Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
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Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yakamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishia, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuahida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishia, Saito, K., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Genome Res. 16 (1), 55-65 (2006)
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340 ACTCAAGGGAACTTTTTTTTTTTTTTTGCCCATAGCCGATTTACTCGTTGGAGGTTTT 399
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                                                                                         400 TGTATTCCGGTTTATATCCCCTATGTCATTACCGGCGAGTGGAGACTCGGACGAGGTCTT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 -----LysAspCysGluProGlyPheValThrGluTrpTyrIleLeuThrIleThrMet 181
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                       107 LeulleSerTyrAspArgTyrGlnSerValSerAsnAlaValSerTyrArgAlaGlnHis
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                                                                                                                                                                                                                                                                                                                                       127 ThrGlyIleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuVal
                                                                                                                                              87 CysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                      147 AsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThr-----
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/mol_type="mRNA"
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Helix Research Institute
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Fax: 81-438-52-3986
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Marra. Bioinformatics: Centre for Biomedical Research, University
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                                                                                                                                              497 TACAACTIGGTÁCTTCCTCATCACGGCTTCCTGGAGTTCTTTACGCCCTTCCTCAGC 556
  157 TrpLys------AsnSerThrAsnThrLysAspCysGluProGlyPheVal 171
                                                                                                   172 ThrGluTrpTyrIleLeuThrIleThrMetLeuLeuGluPheLeuLeuProValIleSer 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="seal_rgb2_575_176_rev"
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/clone_lib="rgb2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koop, B.F., Davidson, W.S. and cGRASP Consortium.
Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
Unpublished (2006)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3NS, Canada
Tel: 250 472 4057
Fax: 250 472 4075
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Matches:
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Insert Length: 791 Std Error: 0.00
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Location/Qualifiers
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Centre for Biomedical Research
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                                                                                                                                                                                                                                                                                                                                                                                              Salmo salar (Atlantic salmon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                            DW582260.1 GI:85054082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bkoop@uvic.ca
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63.48
46.98
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9
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TITLE
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DW582260
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 SerGly1leCysMetPheTrpLeulleThrAspTyrLeuLeuCysThrAlaSerValTyr 103
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                                            Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M Marra. Bioinformatics: Centre for Biomedical Research, University of Victoria Jong Leong, BF Koop.
Insert Length: 542 Std Error: 0.00
Plate: 566
Seq primer: M13 Reverse
High quality sequence stop: 542.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 AGCATCGTTCCTGCCGACGAGTGTTTCGCTGAGTTCTACTGCACCTGGTACTTCCTACTC
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423.00
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 Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                   GCCTTCTGCATCCCACTGTATGTACCTACGTGCTGACAGGCCGCTGGACCTTCGGCCGG 120
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Salmo salar
Salmo salar
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 542)
Koop, B.F. Davidson, W.S. and cGRASP Consortium.
Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
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                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCGCACCCAGAACAACTTCTTCCTGCTCAACCTCGCCATCTCCGACTTTCCTCGTCGC
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Centre for Blomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
                                                                                                                574
24
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3
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Matches:
Conservative:
Mismatches:
Indels:
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
                                                                  ORIGIN
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DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

AUTHORS

REFERENCE

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CB556920 672 bp mRNA linear EST 02-APR-2003
AMGNNUC:URGP1-00001-D6-A urgpl (14349) Rattus norvegicus CDNA clone
urgpl-0001-d6 5', mRNA sequence.
CB556920
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                                                                           107 LeuileSerTyrAspArgTyrGinSerValSerAsnAlaValSerTyrArgAlaGinHis 126
                                                                                                                                                                                                              127 ThrGlylleMetLysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuVal 146
                                                                                                                                                                                                                                                                                 18 LeuAlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIle 37
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                                      68 SerileProLeuTyrileProHisValLeuPhe---AsnTrpAsnPheGlySerGly1le 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                               87 CysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881
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Mismatches:
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
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DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CAAU 0081 row: n column: 18
Plate: CAAU 0081 row: n column: 18
High quality sequence stop: 706.
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                                                                                                                                 Pimephales promelas Eukaryota; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Pimephales.

1 (bass 1 to 728)

1 (bass 1 to 728)

1 (bass 1 to 728)

2 (bass 1 to 728)

3 (bass 1 to 728)

4 Erokstein, P. and Lindquist, E.A.

5 DOE Joint Genome Institute Pimephales promelas EST project
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JGI_CAAU8039.fwd CAAU Pimephales promelas brain 7-8 month adults, males and females pooled (L) Pimephales promelas cDNA clone CAAU8039 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cdna@jgi-psf.org
cDNA Library Preparation: DOE Joint Genome Institute:
                                                                                                                                                                                                                                                                                                   Other ESTS: JGI_CAAU8039.rev
Contact: Lindquist,E.A., Richardson,P.
DOB Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5710
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Matches:
Conservative:
Mismatches:
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/db_xref="taxon:90988"
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DKFZp459P0517).
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/clone_lib="459 (synonym: pcor1). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
                                                                                                                          116
                                                                              CTGTGTGCCTCCTCGGTCTTCAACATCGTACTCATCAGCTATGACCGATTCCTGTCAGTC 526
                                                                                                                                                                                                                                                                               637
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                                                                                                                                                                                                                  ACTCGAGCTGTCTCCTACAGGGCCCAGCAGGGGGACACGAGGCCGCTCGGAAGATG 586
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;

Hominidae; Pongo.

1 (bases 1 to 2633)

Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,

Fobo, G., Han, M. and Wiemann, S.
   77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp459P0517
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Heinrich-Heinne-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp5590617) is available at the RZPD Deutsches Reseourcenzentrum fuer Genomeorschung GmbH in Berlin, Germany Please contact RZPD for ordering:
                                                                                                                          LeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerVal
AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu
                                Phe---AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu
                                                                                                                                                                                                                                                                  GCACTGGTGTGGGTGCTGCTTCCTGCTGTATGGGCCTGCCATCCTG------AGT
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Neuherberg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                              CK859546 2633 bp mRNA linear Pongo pygmaeus mRNA; cDNA DKFZp459P0517 (from clone CR859546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="CAH91711.1"
/db_xref="G1:55729971"
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/note="cholinergic receptor,
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/mol_type="mRNA"
/db_xref="taxon:9600"
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/translation="MNTSAPPAVSPNITVLAPGKGPWQVAFIGITTGLLSLATVTGNL
LVLISFKVNTELKTVNNYFLLSLACADLIIGTFSMULYTTVLMGHWALGTLACDLML
LALDYNASNANNLLLISFORYFSVTRPLSYPAKRTPRRAALMIGLAMLVSFVLMAPA
ILFWQYLVGERTVALGGCYY QFLSOPIITFGTAMAAFYLPVTWGTLYWRIYETESR
ARELAALQGSETPGKGGGSSSSERSOPGAEGSPGTPPGKCCRCRAPRLLQASWKE
EEEBDEGSWESLISSEGEEPGSEVVIKMPWUDFBAQAPTKOPPRSSPNTVKRPTKKGR
DCVPETLMELGYMLCYVNSTINPMCYALGNKARARTLSAILLAFILLWTPYNIMVLVSTFCK
SVHRTPSRQC"
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225 AlaSer------

------SerArgCysProSerHisAlaGlyPheSerThrThrSerSer

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                      Tetcher, V. F., Takubinga, Y., Futaki, S., Garibolai, M.,
Georgii-Hemming, P., Gingerae, T.R., Gojobori, T., Green, R. E.,
Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N.,
Hill, D., Huminiecki, L., Iacono, M., Ikeo, K., Iamaa, A., Ishikawa, T.,
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Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J.,
Liuni, S., Morilliam, S., Miki, H., Mignone, F., Miyake, S.,
Morris, K., Mottagui-Tabar, S., Miki, H., Mignone, F., Miyake, S.,
Morris, K., Mottagui-Tabar, S., Miki, H., Mignone, F., Miyake, S.,
Nilsson, R., Nishiguchi, S., Nori, F., Ohara, O.,
Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavasi, G.,
Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z.,
Ringwald, M., Rost, B., Ruan, Y., Shimada, H., Shimada, K., Silva, D.,
Schneider, C., Schonbach, C., Sekiguchi, K., Sandelin, A.,
Schneider, C., Schonbach, C., Sekiguchi, K., Sandelin, A.,
Sensaki, Y., Taki, K., Tamaoja, K., Tan, S.L., Tang, S., Taylor, M.S.,
Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S.,
Hide, W., Bult, C., Grimmond, S. M., Tasdale, R.D., Liu, E.T.,
Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A.,
Kal, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Karyama, M.,
Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M.,
Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M.,
Kato, T., Kawaji, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M.,
Plessy, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K.,
Watahiki, A., Okamura, N., Shiraki, T., Suzuki, S., Tagami, M., Waki, K.,
Watahiki, A., Okamura, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K.,
Watahiki, A., Okamura, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K.,
Watahiki, A., Okamura, K., Shiraki, T., Suzuki, S., Tagami, Y., Congortium
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Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K.,
Hori, F., Iida, J., Imamura, K., Imotani, W., Itoh, W., Kamana, J.,
Kawai, J., Kolima, M., Konno, H., Maramura, M., Nakamura, M., Ninomiya, N.,
Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D.,
Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

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URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
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       Futaki,S.,
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Please visit our web site for further details.
Please visit our web site ior further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Fletcher, C.F., Fukushima, T., Furuno, M.,
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/strain="C57BL/6J"
/db xref="FANTOM DB
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ARELAALQGSETPGKGGSSSSSERSQPGAEGSPESPPGRCCRCCRAPRLLQAYSWKE
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                    527. 1909
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muscarinic 1, CNS (MGD|MGI:88396 GB|NM_007698, evidence:
BLASTN, 100%, match=2619)
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ARELAALQGSETPGRGGSSSSERSQPGAEGSPESPERFCRCRCRAPRLLQAYSWKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LysAsnSerThrAsnThrLysAspCysGluProGlyPheValThrGluTrpTyrIleLe 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uThrlleThrMetLeuLeuGluPheLeuLeuProVallleSerValAlaTyrPheAsnVa 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
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124
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Indels:
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                                                sex="male
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DB:
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Mismatches:
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Gaps:
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Matches:
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Facent No. 6204017
GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Honsam M.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Monsma, Frederick J. Jr.
APPLICANT: Wang, Suke
FILEANT: Umland, Shelby P.
APPLICANT: Wang, Suke
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/414,010
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
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Query Match:
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LENGTH: 1173
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Matches:
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APPLICANT: Behan, Jiang Xu
APPLICANT: Laz, Thomas M.
APPLICANT: Laz, Thomas M.
APPLICANT: Monsem, Frederick J. Jr.
APPLICANT: Morse, Kelley L.
APPLICANT: Morse, Kelley L.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CNOIO69
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/414,010
PRIOR FILING DATE: 1999-10-07
                                                                                                                                                                                               ; Sequence 1, Application US/09812216; Patent No. 6613533; GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
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NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
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APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENOSO
CURRENT APPLICATION NUMBER: US/09/875,076
CURRENT FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/417,044
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
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Matches:
PRIOR APPLICATION NUMBER: 60/123,949
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-05-28
PRIOR PELING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR PELING DATE: 1999-05-28
PRIOR PELING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR PELING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/137,127
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR APPLICATION NUMBER: 60/137,131
PRIOR PELING DATE: 1999-05-29
PRIOR PILING DATE: 1999-05-29
PRIOR PELING DATE: 1999-02-29
PRIOR PELING DATE: 1999-09-29
PRIOR PILING DATE: 1999-09-29
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PRIOR PILING DATE: 1999-00-19
PRIOR PILING DATE: 1999-10-01
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 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND UPILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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Sequence 5059, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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LENGTH: 2665
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48.9%
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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291..1625
                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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Best Local Similarity:
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LOCATION:
                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                        US-08-985-090-1
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                                   1171 GGCGGTGGGGGC------GGCTCCGTGGCTTCACCCACCTCCAGCTCCGGC--- 1215
                                                                                                                                                         -----TCACTCAAGAGGGCTCCAAGCCTCCAAGAGGGGCTCCAAGCCGTCG 1272
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   SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
                                                                 244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal
                                                                                                                           SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg
                                                                                                                                                                                                                                                    295 AlaGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPhe
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Patent No. 5885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                 -----AGCTCCTCGAGGGCACTGAGAGGCCGCGC-----
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21P: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ANTWARE: TACENTY Release #1.0, Version #1.25
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STREET: 28 State Street
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APPLICATION NUMBER: US/08/985,090
FILING DATE:
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REGISTRATION NUMBER: 39,030
REPERENCE/DOCKET NUMBER: MNI-032
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-985-090-1
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1110 AGGTATGGGGTGGGTGAGGCGGCCGTAGGCGCTGAGGCGAGGCGACCCTCGGGGGT 1169
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Length:
Matches:
Conservative:
Mismatches:
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1170 GGCGGTGGGGGC------GGCTCCGTGGCTTCACCCACCTCCAGCTCCGGC--- 1214
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1272 GCGTCCTCGGCCTCGAGAAGGCGCATGAAGATGGTGTCCCAGAGCTTCACCCAGGGC 1331
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                                                                                                                                                                      264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
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224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
                                                                                                                                                                                                                                                            284 SerGluSerAlaAlaLeuArgGlnArg-----------GluTyr 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluargProLysSerValTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPhe 354
                                                                                     244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal
                                                                                                                            1215 -----AGCTCCTCGAGGGCACTGAGAGGCCGCGC------AGCTCCTCGAGGGCACTGAGAGGCCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor NUMBER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/165,543
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APPLICATION NUMBER: 09/042,780
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Patent No. 6093545
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
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COUNTRY:
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990 GATGGGGCTCGAGGGAGGCAGCCCCGAGCCCCTCCCGAGGCCCAGCCCTCACCACCC 1049
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Indels:
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Matches:
            TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                         LENGTH: 2689 base pairs
TYPE: nucleic acid
STRANDEDDESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
(617)227-7400
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938 GTCACCTTCTTTAACCTCGAGCATCTGAACATCCAGAGGCGCACCCGCCTCCGGCTG 997
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                                                                  ------TCACTCAAGAGGGGCTCCAAGCCGTCG 1271
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GCGTCCTCGGCCTCACTGGAGAAGGGCATGAAGATGGTGTCCCAGAGCTTCACCCAGGGC 1331
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APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree
APPLICANT: HUVAT: Arne
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
WUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 2699
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	380 1636	RESULT 8 US-09-642-855-5 Sequence 5, Application US/09642855 Patent No. 6413743 GENERAL INFORMATION: APPLICANT: Lovenberg, Timothy APPLICANT: Briander, Mark APPLICANT: Pyati, Jayashree APPLICANT: Arne TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3 Db	/642,855 354 of Artificial Sequence: CDNA	Alignment Scores:  Pred. No.:  Score:  Pred. No.:  Score:  Pact So Matches:  Best Local Similarity:  35.4\$ Conservative: 52  Best Local Similarity:  35.4\$ Mismatches:  115  Guery Match:  35.4\$ Mismatches:  116  Gaps:  12  US-10-626-445-8 (1-391) x US-09-642-855-5 (1-2699)  Cy 18 LeualaPheLeuMetSerSerPheAlaTleMetValGlyAsnAlaValValIle 37  Cy 18 LeualaPheValValAspArgAnaTleMetValGlyAsnAlaValValIle 37  Cy 38 LeualaPheValValAspArgAnaLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57  Cy 38 LeualaPheValValAspArgAnaLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57  Cy 38 LeualaPheValValAspArgAnaNathaNaphisArgSerAsnTyrPhePheLeuAsnLeu 57  Cy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77  Cy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeu 77  Cy 58 AlaIleSerAspPheLeuValGlyLeuIleSerIleProLeuTyrIleu 96  Cy 78 PheAsnTrpAsnPheGlySerGlyIleCyMetPheTrpLeuIleThrAspTyLeu 96  Cy 78 PheAsnTrpAsnPheGlySerGlyIle 11

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               878 TACAACTGGTACTTCCTCATCACGCTTCCACCCTGGAGTTCTTTACGCCCTTCCTCAGC 937
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Sequence 5, Application US/09642852

GENERAL INFORMATION:
APPLICANT: Erlander, Mark
APPLICANT: Bridger, Mark
APPLICANT: Huvar, Arne
TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF TITLE REPERENCE: JWW
TITLE OF INVENTION: SUBTYPE
FILE REPERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/642,852
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                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Exlander, Mark
APPLICANT: Exlander, Mark
APPLICANT: Exlander, Mark
APPLICANT: PAYEL, JAyashree
TITLE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: ORTI1290
CURRENT APPLICATION NUMBER: US/09/642,514
FILE REFERENCE: ORTI1290
CURRENT APPLICATION NUMBER: US 09/167,354
PRIOR APPLICATION NUMBER: US 09/167,354
PRIOR APPLICATION NUMBER: US 09/167,354
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 5:
LENGTH: 2699
                              ; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-514-5
             -----SroAlaLeuSerGlnAsnGlnSer
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Matches:
Conservative:
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Best Local Similarity:
Query Match:
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1118 AGGTATGGGGTGGGTGAGGCGGCCGTAGGCGCTGAGGCCGGGGGAGGCGACCCTCGGGGGT 1177
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28 State Street
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REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5885893
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APPLICATION NUMBER:
FILING DATE:
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STREET: 28
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                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: CDNA
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: 09/167,354
PRIOR FILING DATE: 1998-10-07
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48.9%
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                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                            NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 2699
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224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu 243
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APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
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                                                                                                                                                                                                        264 SerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrpArg 283
                                                                                                                                                                                                                                          ------TCACTCAAGAGGGGCTCCAAGCCGTCG 981
                                                                                   AGGTATGGGGTGGGTGAGGCGGTGAGGCGCTGAGGCCGGGGGAGGCGACCCTCGGGGGT
                                                          224 SerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeu
                                                                                                                                244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal
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Patent No. 6093545

GENERAL INFORMATION:

APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman

TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSER: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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NAME: Elizabeth A. Hanley
RECISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
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STATE: Massachusetts
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520 TGGGAGTACCTGTCCGGGGGCATCCCCGAGGGCCACTGCTATGCCGAGTTCTTC
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                                                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                              Length:
TELEPAX: (617)227-7400
TELEFAX: (617)742-4214
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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722.50
50.8%
38.8%
35.3%
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Best Local Similarity:
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; LOCATION:
US-08-985-090-3
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Pred. No.:
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315 AlalleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrProArgThr 334
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                                                                                  244 LysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeuVal
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                                                                                                                                                                                        ------TCACTCAAGAGGGCTCCAAGCGTCG
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                                              880 GGCGGTGGGGGC-----GGCTCCGTGGCTTCACCCACCTCCAGCTCCGGC---
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APPLICANT: Lovenberg, Timothy
APPLICANT: Exlander, Mark
APPLICANT: Exlander, Mark
APPLICANT: Huvar, Arne
TITLE OF INVENTION: SUBTYPE
FILE REPRENCE: UWW
CURRENT APPLICATION NUMBER: US/09/167,354A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 8
CORPENDED: PRESET 100: 100: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: CDNA
                                                                                                       ----AGCTCCTCGAGGGCACTGAGAGGCCGCGC
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Mismatches:
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722.50
50.8%
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35.3%
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SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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Matches:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                             2.89e-65
                                                                                                                                                                                                                                    722.50
50.8%
38.8%
35.3%
                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity:
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US-09-165-543-3
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APPLICANT: Extander, Mark
APPLICANT: Extander, Mark
APPLICANT: Prati, Jayashree
APPLICANT: Pyati, Jayashree
TITUE OF INVENTION: SUBTYPE
TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: JWW
CURRENT APPLICATION NUMBER: US/09/642,855
CURRENT APPLICATION NUMBER: 09/167,354
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFWARE: Patentin Ver. 2.0
SEQ ID NOS: 8
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Conservative:
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ORGANISM: Artificial Sequence
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US-09-642-514-6
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Mismatches:
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                          TITLE OF INVENTION: SUBTYPE
FILE REFERENCE: ORT1290
CURRENT APPLICATION NUMBER: US/09/642,514
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 09/167,354
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Patent No. 6437100
GENERAL INFORMATION:
APPLICANT: Lovenberg, Timothy
APPLICANT: Erlander, Mark
APPLICANT: Pyati, Jayashree
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Sequence 5, Application US/10626445
Fublication No. US200402482521
GENERAL INFORMATION:
GENERAL INFORMATION:
THIRD TAPLICANT: Liu, Changlu
TITLE OF INVENTION:
TITLE OF INVENTION DAMA Encoding Mammalian Histamine Receptor Of The H4 Subtype
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/626,445
CURRENT PILING DATE: 2003-07-23
FRIOR PLILING DATE: 2001-02-22
FRIOR APPLICATION NUMBER: 60/208,260
FRIOR APPLICATION NUMBER: 60/208,260
FRIOR PILING DATE: 2000-05-31
FRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
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US-09-852-165-1

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US-10-290-078-25

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US-09-910-411-1

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US-09-876-252-13

US-10-052-193-1

US-10-254-293-13

US-10-354-76-11

US-10-417-820A-13

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US-10-417-820A-13

US-10-782-596-13

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ORGANISM: Mus musculus
US-10-626-445-5
 Alignment Scores:
Pred. No.:
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   Published Applications NA Main:*

1. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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                   GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                           OM protein - nucleic search, using frame_plus_p2n model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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	Db 1081 CCTTGGTGTCAGGGGTTTCCAGAGGGTTTCTGGAAGGTACT  Qy 381 ProAlaLeuSerGlnAsnGlnSerValSerSer 391	RESULT 2 US-10-626-126-5 ; Sequence 5, Application US/10626126 ; Publication No. US20050074770A1 ; GENERAL INFORMATION: ; APPLICANT: Lovenberg, Timothy ; APPLICANT: Liu, Changlu ; TITLE OF INVENTION: DNAS Encoding Mammalian Histamine R	CURRENT FALLATION NUMBER: US/10/626,126 CURRENT FILING DATE: 2003-07-23 PRIOR APPLICATION NUMBER: 09/790,849 PRIOR APPLICATION NUMBER: 09/790,849 PRIOR APPLICATION NUMBER: 60/208,260 PRIOR APPLICATION NUMBER: 60/208,260 PRIOR FILING DATE: 2000-05-31 NUMBER OF SEQ ID NOS: 27	; SOFTWAKE: PACENTIN VETBION 3.2 ; SEQ ID NO 5 ; LENGTH: 1176 ; TYPE: DNA ; ORGANISM: Mus musculus US-10-626-126-5	Scores: 1.91e-214 2035.00 imilarity: 99.7* ch: 10.4*	US-10-626-445-8 (1-391) X US-10-626-126-5 (1-1176)  Qy	21	Qy 41 ValvalAspArgAsnLeuArgHisArgSerAsnTyrPhePheLe	Db 181 GACTTCCTCGTGGGTTTGATTTCCATTCCTCTGTACATCCCTCA Qy 81 AsnPheGlySerGly1leCy8MetPheTrpLeulleThrAspTy Db 241 AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGATTACTGACTA	Oy 101 SerValTyrAsnileValLeuileSerTyrAspArgTyrGlnSe
ore: 2035.00 Matches: 390 rent Similarity: 99.7% Conservative: 0 er Local Similarity: 99.7% Mismatches: 1 ery Match: 99.4% Indels: 0 : -10-626-445-8 (1-391) x US-10-626-445-5 (1-1176)	Qy         1 MetSerGluSerAsnSerThrGlyIleLeuProbroAlaAlaGlnValProJeuAlaPhe 20           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         41 ValvalAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60           Db         121 GrGGTGGACAGAAACCTTAGACATCGAAGTAATTTTTTTTTT	Qy         81 AsnPheGlySerGlyIleCysMetPheTrpLeulleThrAspTyrLeuLeuCysThrAla 100           Db         241 AATTTTGGAAGTGGAATCTGCATGTTTTGGCTCATTACTGACTATCTTTTGTGCACGCA 300           Qy         101 SerValTyrAsnIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120           Db         301 TCTGTCTACAATATTGTCCTCATTAGCTACGATACCAGTCAGT	Qy         121 SerTyrArgAlaGlnHisThrGlyIleMetLysIleValAlaGlnMetValAlaValTrp 140           DS         361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATGGTGGTGTTTGG 420           Qy         141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160	421 ATACTGGCTTTCTTGGTAATGGCCCGATGATTCTGGGCTTCAGATTCTTGGAAGAACAGC 161 ThrasnThriysAspCysGluProGlyPheValThrGluTrpTyrileLeuThrileThr	Db 541 ATGCTCTTGGAATTCCTGCTTCCTGTTCTTGTGGCTTATTTCAATGTACAGATTTAC 600 Qy 201 TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr 220	ThrSerSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsn 	Qy 241 ProGlyLeuLygGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer 260		Oy 301 ArglysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320

 96 qa	
	TrpTyrSerileAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
 Db 1021	TGGTACAGCATTGCCTTCTGGCTGCAATGGTTCAATTCGTTTGTTAATCCTTTCTGTAC
 Qy 36 Db 108	361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380 
 Qy 38 Db 114	381 ProAlaLeuSerGlnAsnGlnSerValSerSer         391
RESULT 2 US-10-626-126- Sequence 5, Publication GENERAL INFO: APPLICANT: APPL	RESULT 2 US-10-626-126-5 Sequence 5, Application US/10626126 Sequence 5, Application No. US2005074770A1 Sequence 5, Application No. US2005074770A1 SEQUENCE 1
 Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	1.91e-214   Length: 1176   2035.00   Matches: 390   39.7%   Conservative: 0   Similarity: 99.7%   Mismatches: 1   19.4%   Indels: 0   10   Gaps: 0
 US-10-626-44	-445-8 (1-391) x US-10-626-126-5 (1-1176)
Çy Bb	1 MetSerGluserAsnSerThrGlylleLeuProProAlaAlaGlnValProLeuAlaPhe 20
Oy 2 Db 6	21 LeumetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe 40 
Oy 4 Db 12	41 ValValAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60 
 Oy 6 Db 18	61 AspPheLeuValGlyLeuIleSerIleProLeuTyrIleProHisValLeuPheAsnTrp 80 
 Oy 8 Db 24	81 AsnPheGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100 
 Oy 10	101 ServalTyrAsnileValLeuileSerTyrAspArgTyrGinSerValSerAsnAlaVal 120 
	01 ICIGLIALAHIATIOICCICAHIAGARANGA CARANGANA C

J.ENGTH: 1176   TYPE: DNA   CNCANUSM: Mus musculus   JS-10-626-398-5   Alignment Scores:	Oy 1 Met.SerGlusserAsnSerThrGly1leLeuProProAlaAlaGlnValProLeuAlaPhe 20	1 TTAATGTCTTCATTTGCTATTATTGTT	Oy 61 AspPheLeuValGlyLeulleSerIleProLeuTyrlleProHisValLeuPheAsnTrp 80	Db 241 AATTTTGGAAGTGGAATCTGCATTTTTTTTTTTTTTTTT	Oy 121 SerTyrArgAlaGlnHieThrGlylleMetLyslleValAlaGlnMetValAlaValTrp 140		Qy 161 ThrAsmThrLysAspCysGluFroGlyPheValThrGluTrpTyrIleLeuThrIleThr 180 	Qy 181 MetLeuLeuGluPheLeuLeuProValIleSerValAlaTyrPheAsnValGlnIleTyr 200	Oy 201 TrpSerLeuTrpLy8ArgArgAlaLeuSerArgCy8ProSerHisAlaGlyPheSerThr 220
Db 361 TCTTATAGGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAAATGGTGGCTGTTTGG 420  Qy 141 IleLeualaPheLeuValAsnGlyProMetIleLeualaSerAspSerTrpLysAsnSer 160  421 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTCTTGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	Oy 201 TrpSerLeuTrpLysArgalaLeuSerArgCysProSerHisAlaGlyPheSerThr 220	661 ACCTCTTCCAGTGCTTCAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAGTAAT  241 ProGlyLeuLy8GluSerAlaAlaSerArgHisSerGluSerProArgArglysSerSer  11	Oy 261 IleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySer 280	Db 841 TTCTGGCATCGGAAGGCTTCGCCAAAGGAGTACGCAGAGCTTCTCAGAGGC 900  Qy 301 ArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  Db 901 AGGAAGCTAGCCAGGTCATCGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGAGCTCA 960	Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal 340 	Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360 	Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrp 380 	Qy         381 ProalaLeuSerGlnAsnGlnSerValSerSer         391	RESULT 3 US-10-626-398-5 Sequence 5, Application US/10626398 Sequence 5, Application US/10626398 Sequence 5, Application No. US20050074841A1 GENERAL INFORMATION: APPLICANT: Lovenberg, Timothy APPLICANT: Liu, Changlu TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype TITLE OF INVENTION: UNMBER: US/10/626,398 CURRENT APPLICATION NUMBER: US/10/626,398 CURRENT FILING DATE: 2003-07-23 FRIOR APPLICATION NUMBER: 60/790,849 PRIOR FILING DATE: 2001-02-22 FRIOR APPLICATION NUMBER: 60/208,260 FRIOR FILING DATE: 2000-05-31 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin Version 3.2 SEQ ID NO 5

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Sequence 6, Application US/10626126 Publication No. US20050074770A1 GENERAL INFORMATION:
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                      ArglysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
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TTCTGGCGATCGGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC
                                    AGGAAGCTAGCCAGGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTTGCTGGGCTCCA
                                                                      TyrCysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerVal
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                                                                                                                                                                                                                                                                                                              APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DAS Encoding Mammalian Histamine Receptor Of The FILE REPERENCE: PRO-0032
CURRENT APPLICATION NUMBER: US/10/626,445
CURRENT FILING DATE: 2003-07-23
PRIOR PRILICATION NUMBER: 09/790,849
PRIOR PILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Lovenberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAS Encoding Mammalian Histamine Receptor Of The H4 Subtype
TILE REFERENCE: PRD-0033
CURRENT APPLICATION NUMBER: US/10/626,126
CURRENT FILING DATE: 2003-07-23
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us-10-626-445-8.p2n.rnpbm

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APPLICANT: Lovelberg, Timothy
APPLICANT: Liu, Changlu
TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype;
FILE REFERENCE: PRD-0034
CURRENT APPLICATION NUMBER: US/10/626,398
CURRENT FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: 60/208,260
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LEASTH 1176
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; Publication No. US20050074841A1
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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PRIOR APPLICATION NUMBER: 09/790,849
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/208,260
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PALENTIN VETSION 3.2
SEO ID NO 6
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                                                                                                TYPE: DNA ORGANISM: Rattus
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Best Local Similarity:
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; OTHER INFORMATION: Jones - Genbank Accession No.: AF307973; Nucleotides 460-462
; OTHER INFORMATION: are AAG and 988 is C
US-10-488-421-7
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OTHER INFORMATION: Nguyen, et al., Mol. Pharmacol 59(3):427-433 (2001) a.a.
OTHER INFORMATION: only
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NAME/KEY: misc_feature
OTHER INFORMATION: Banyu - Genbank Accession No.: AB045370; WO 01/46414
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NAME/EXT: misc feature
OTHER INFORMATION: Liu - Genbank Accession No. AF312230 - Liu
OTHER INFORMATION: Pharmacol 59(3):420-426 (2001)
APPLICANT: Merck & Co., Inc. [US/US]
APPLICANT: Gallagher, Michael J.
APPLICANT: Gallagher, Michael J.
TITLE OF INVENTION: HISTAMINE RECEPTOR H4 POLYNUCLEOTIDES
FILE REPERENCE: 1367-133354001
CURRENT APPLICATION NUMBER: US/10/488,421
CURRENT FILING DATE: 2004-03-01
PRIOR APPLICATION NUMBER: US 60/316,762
PRIOR APPLICATION NUMBER: US 60/332,697
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
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OTHER INFORMATION: Morse, et al., JPET 296(3):1058-1066
OTHER INFORMATION: No. 6,204,017; WO 01/25432 A2
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LOCATION: (1)..(1170)
OTHER INFORMATION:
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Sequence 1, Application US/09812216
Patent No. US20020098539A1
GENERAL INFORMATION:
APPLICANT: Behan, Jiang Xu
APPLICANT: Hedrick, Joseph A.
APPLICANT: Monsma, Frederick J. Jr.

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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Umland, Shelby P.
APPLICANT: Wang, Suke
TITLE OF INVENTION: Histamine receptor
FILE REFERENCE: CN01069
CURRENT APPLICATION NUMBER: US/09/812,216
CURRENT FILING DATE: 2001-03-19
PRIOR PILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                           9.05e-141
1370.50
78.3$
68.1$
                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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Query Match:
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                        715 TCTGCATCGACAĞAAGTTCCTĞCATCCTTTCATTCAĞAĞAGACAGAĞAĞAAAĞAĞTAGT 774
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ProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSer
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APPLICANT: L1, Xiatong
APPLICANT: L2, Xiatong
APPLICANT: Achalovich, David
APPLICANT: Zhu, Yuan
APPLICANT: Zhu, Yuan
TITLE OF INVENTION ANORES: US/09/910,411
CURRENT APPLICATION NUMBER: US/09/910,411
CURRENT APPLICATION NUMBER: 09/693,761
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/497,790
PRIOR FILING DATE: 2000-20-3
PRIOR PILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FRSESEQ for Windows Version 4.0
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Patent No. US20020137054A1
GENERAL INFORMATION:
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ORGANISM: Homo sapien
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Best Local Similarity:
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Pred. No.:
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                                           21 LeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaValValIleLeuAlaPhe
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Query Match:
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| Publication No. US2030017528A1
| GRUERAL INFORMATION: | House T. |
| APPLICANT: Chen, Rucping T. |
| APPLICANT: Chen, Rucping T. |
| APPLICANT: Lida, Chen W. |
| FRIOR PLICATION NUMBER: US/12, 946 |
| PRIOR PLICATION NUMBER: US/12, 946 |
| PRIOR PLICATION NUMBER: US/13, 946 |
| PRIOR PLICANT: LIDAD DATE: 1999-02-12 |
| PRIOR PLICANT: UNIVER: US/13, 946 |
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Matches:
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ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60/156,555
PRIOR FILING DATE: 1999-09-29;
PRIOR PELLING DATE: 1999-09-29;
PRIOR PELLING DATE: 1999-09-29;
PRIOR FILING DATE: 1999-09-29;
PRIOR FILING DATE: 1999-09-29;
PRIOR PILING DATE: 1999-10-01;
PRIOR PILING DATE: 1999-10-01;
PRIOR PILING DATE: 1999-10-01;
PRIOR PILING DATE: 1999-10-01;
PRIOR APPLICATION NUMBER: 60/157,281;
PRIOR APPLICATION NUMBER: 60/157,281;
PRIOR FILING DATE: 1999-10-01;
PRIOR PILING DATE: 1999-10-01;
PRIOR PILING DATE: 1999-10-01;
PRIOR FILING DATE: 1999-10-01;
PRIOR FILING DATE: 1999-10-01;
PRIOR FILING DATE: 1999-00-10;
PRIOR FILING DATE: 1999-00-10;
PRIOR FILING DATE: 1999-00-29;
NUMBER OF SEQ ID NOS: 146;
SOFTWARE: PALENTIN VERSION 3.0;
LENGTH 1173
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ORGANISM: Homo sapiens
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Query Match:
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APPLICANT: LOMAITE, Kevin P.
APPLICANT: Lin, Lin
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APPLICANT: Chen, Ruoping
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T.
APPLICANT: Chen, Ruoping
TILE REPERSENCE: AREN-0054
TILE REPERSENCE: AREN-0054
CURRENT APPLICATION NUMBER: US/09/876,252
CURRENT APPLICATION NUMBER: US/09/876,252
CURRENT FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/110,060
PRIOR PLING DATE: 1999-02-16
PRIOR PLING DATE: 1999-02-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-13
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              TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
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R APPLICATION NUMBER: 60/108,029

R FILING DATE: 1998-11-12

R APPLICATION NUMBER: 60/136,436

R FILING DATE: 1999-06-28

R APPLICATION NUMBER: 60/136,439
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APPLICATION NUMBER: 60/141,448
FILING DATE: 1999-06-29
APPLICATION NUMBER: 60/136,437
FILING DATE: 1999-05-28
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APPLICATION NUMBER: 60/136,567
FILING DATE: 1999-05-28
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APPLICATION NUMBER: 60/137,131
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APPLICATION NUMBER: 60/152,524
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                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09876252 Publication No. US20030018182A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             Karin
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            TrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSerThr
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; Publication No. US20020132755A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PCLO963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT PLING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR PLING DATE: 2001-01-17
; WINGER OF SEQ 1D NOS: 10
; SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity:
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APPLICANT: O'Keilly, Mark A.
APPLICANT: O'Keilly, Mark A.
TITLE OF INVENTION: NOVEL POLYPEPTIDE
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    See File Wrapper or PALM.

                                                                                                                                                                                              APPLICANT: Dang, Huōng<sup>T</sup>T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, 1-Lin
TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
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                                      Conservative:
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Matches:
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CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 2002-10-17
CURRENT FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: US/09/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-16
PRIOR FILING DATE: 1999-02-16
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
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PRIOR FILING DATE: 1999-05-28
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                                                                                                                                                                             APPLICANT: Chen, Ruoping APPLICANT: Dang, Huong T
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ORGANISM: Homo sapiens
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161 ThrasnThrLysAspCysGluProGlyPheValThrGluTrpTyrlleLeuThrlleThr
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APPLICANT: Chen, Ruoping
APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
TITLE REFERENCE: ARENOGSO
CURRENT FILING DATE: 2003-03-21
PRIOR PLICATION NUMBER: US/10/393,807
CURRENT FILING DATE: 1999-10-12
PRIOR PLICATION NUMBER: 60/109,213
PRIOR PLILING DATE: 1999-10-12
PRIOR PLILING DATE: 1999-10-26
PRIOR PLILING DATE: 1999-02-26
PRIOR PLILING DATE: 1999-02-26
PRIOR PLILING DATE: 1999-03-22
PRIOR PLILING DATE: 1999-03-12
PRIOR PLILING DATE: 1999-05-28
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Matches:
Conservative:
Mismatches:
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FILE REFERENCE: PC10373B
CURRENT APPLICATION NUMBER: US/10/354,769
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 09/698,801
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: 1999-10-29
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
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ORGANISM: Homo sapiens
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          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                         Percent Similarity:
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                                                         Alignment Scores:
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LENGTH: 1173
                                 US-10-393-807-13
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113, Appl 114, Appl 2, Appli 3, Appli 34, Appli 46, Appl 46, Appl 20, Appl

Sequence:

Run on:

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y APPLICANT: Carroll, Joseph M.

APPLICANT: Carroll, Joseph M.

APPLICANT: Carroll, Joseph M.

APPLICANT: Healy, Aileen

TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hemacological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hemacological Disorders Using 232, 2059, 10630, 14717, 9941, 19310, c
TITLE OF INVENTION: Hemacological Disorders Using 232, 304, 1980, 14717, 9941, 19310, c
FILE REPERENCE: MPIZO10-288PIRCPIOWNIM
CURRENT APPLICATION NUMBER: US/11/242,505A

CURRENT APPLICATION NUMBER: US 10/290,078

PRIOR FILING DATE: 2002-11-07

PRIOR APPLICATION NUMBER: US 10/320,351

PRIOR FILING DATE: 2002-12-16

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/341,606

PRIOR FILING DATE: 2001-12-17

NUMBER OF SEQ ID NOS: 48

SEGFWARE: FastSEQ for Windows Version 4.0
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US-11-302-678-21

US-11-302-678-19

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US-11-302-678-36

US-10-511-937-2918

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US-11-125-851A-72

US-11-25-851A-72
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     TYPE: DNA
ORGANISM: HOMO
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       Command line parameters:
-MODEL=trame+.p2n.model.-DEV=xlp
-Q=/abss/ABSSWEB_spool/US10626445/runat_24052006_100010_14056/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US10626445/runat_24052006_100010_14056/app_query.fasta_1
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITG=b1ts -START=1 -END=-1 -MATRIX=blosum62
-LOOPCL=0 -LOOPEXT=0 -UNITG=b1ts -START=1 -CONDER=Ct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LCCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -HOST=abss03p
-NAXIEN=2000000000 -HOST=abss03p
-NO MAAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DBV TIMEOUT=120
-NARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: / EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: / EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: / EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: / EMC_Celerra_SIDS3/ptodata/2/pubpna/DS07_NEW_PUB.seq:*
5: / EMC_Celerra_SIDS3/ptodata/2/pubpna/DS1_NEW_PUB.seq:*
6: / EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: / EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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Sequence 2881,
Sequence 40,
Sequence 39, 1
Sequence 11, 2
Sequence 11, 2
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                           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-242-505A-25
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Mismatches:
Indels:
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               Matches:
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TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310
FILE REFERENCE: MPIZO10-288PIRCPIOMNIM
CURRENT APPLICATION NUMBER: US/11/242,505A
CURRENT FILING DATE: 2005-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-17
PRIOR FILING DATE: 2001-11-17
PRIOR APPLICATION NUMBER: US 60/341,606
PRIOR FILING DATE: 2001-12-17
                                                                                            1075 CCATTGTGTCACAAGCGCTTTCAAAAGGCTTTCTTGAAAATTTTTGTATAAAAAGCAA 1134
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                                                                      TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerPheValAsnProPheLeuTyr 360
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/11242505A; Publication No. US20060099656A1
GENERAL INFORMATION: APPLICANT: CATZOIL, JOSEPH M.
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Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wodward, Robert
APPLICANT: Wodward, Robert
APPLICANT: Wodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
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APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSFLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: US/10/511,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/31,831
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
LENGTH: 1847
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US-10-511-937-2881
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APPLICANT: Venkateswarlu, Karicheti
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: WOLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: MPIO2-012PIRNM ONNI
CURRENT APPLICATION NUMBER: US/11/302,678
CURRENT FILING DATE: 2005-12-14
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                                                         226 rGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGlyLeuLysGluSe 246
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PRIOR PLILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US 60/349,511
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PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-02-8
PRIOR FILING DATE: 2002-03-15
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PRIOR FILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/403,468
PRIOR PILING DATE: 2002-08-14
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; Publication No. US2006008881A1
; GENERAL INFORMATION:
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Publication No. US2006008881A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Venkateswarlu, Karicheti
TITLE OF INVENTION: WELHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: G41, 260, 55089, 21407, 42032, 46656, 6259;
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 6259;
TITLE OF INVENTION: 12203, 985, 13237, 13601, 18926, 318, 2055;
TITLE REPERENCE: MPIOZ-OLIPPIRNM OWNI
CURRENT APPLICATION NUMBER: US/11/302,678
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PRIOR APPLICATION NUMBER: US/10/345,680

PRIOR FILING DATE: 2003-01-16

PRIOR PELING DATE: 2003-01-18

PRIOR FILING DATE: 2002-01-18

PRIOR PLING DATE: 2002-02-28

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NUMBER OF SEQ ID NOS: 66

SOFTWARE: PASESEQ FOR WINDOWS VERSION 4.0

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                                                                                                                                                                                                                                         SerAsnSerThr ----- GlyIleLeuProProAlaAlaGlnValProLeuAlaPhe
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1984
103
65
136
105
                           Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                             21 LeuMetSerSerPheAlaPheAlaIleMetVal----
                                                                                                                                                                                     US-10-626-445-8 (1-391) x US-11-302-678-40 (1-1984)
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                                                                                                           Indels:
     Length:
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Query Match:         14.4%         Indels:         69           DB:         7         Gaps:         14           DB:         10-626-445-8 (1-391) x US-11-302-678-39 (1-1074)         36           QY         18 LeualapheleuwetSerSerbhealaphealailewetvalGlyAsnalavalval 36           Db         139 CTGGGCTTTTCTGGTGGCGGCGACGTTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG		Oy 249 SerArgHisSerGluSerProArgArgLysSerSerIleLeuValSerLeuArgThrHis 268   116
IneuSeralaphe	TITLE OF INVENTION: 12303, 985, 13337, 13601, 18926, 318, 2058 OR 6351 MOLECULES.	FRIOR FILLING DATE: 2002-11-05 FRIOR PELLING DATE: 2002-11-05 FRIOR PEPLICATION NUMBER: US 60/429,797 FRIOR FILLING DATE: 2002-11-26 NUMBER OF SEQ ID NOS: 66 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 39 LENGTH: 1074 TYBE: DNA ORGANISM: Homo Sapiens FEATURE: NAME/KEY: CDS LOCATION: (1)(1074) US-11-302-678-39 Alignment Scores: Pred. No.: 295.50 Matches: Rest Local Similarity: 24.2\$ Mismatches: 134

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1042 GGCTACTCCAACTCCTTTAACCCCCTGATCTATACGGCTTTCAACAAGAACTACAAC 1101
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304 TCCATGGCCGTCTCGGATGTCCTGGTGGCCGCTGGTCATGCCGCTGAGCCTGGTGATGATGTCTGGTGGCTGATGATGTCTGGTGGCCTGGTGGCTGGTCATGCCGCTGGTCATGCCGTGGTCATGCCGTGGTGGTGATGTCTGGTGGCTGGTGGTCATGCCGTGGTCATGCCGTGGTGGTCATGCCGTGGTCATGCCGTGGTGGTGGTGGTGGT
                                                                                                                                                                                                                                                                                                                                                134 AlaGlnMetValAlaVal---TrplleLeuAlaPheLeuValAsnGlyProMetIleLeu 152
                                                                                                                                                                                                                                                                                                                                                                        153 AlaSerAspSerTrpLysAsnSerThrAsnThrLysAspCys------GluPro 168
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                                                                                                                                                                                      ValleuPhe-----AsnTrpAsnPheGlySerGlyIleCysMetPheTrpLeuIleThr
                                                                                                                                                                                                                                                      114 GlnSerValSerAsnAlaValSerTyrArgAlaGlnHisThrGlyIleMetLysIleVal
                                                                                                                                                            AspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeuIleSerTyrAspArgTyr
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y Sequence 16, Application US/11242505A
publication No. US20060099656A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1102 AGCĠĊĊŤŤĊ 1110
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Venkateswarlu, Karichein
TITLE OF INVENTION: WETHODS AND COMPOSITIONS POR TREATING
TITLE OF INVENTION: WELL DISORDERS USING 1183, 559, 34021, 44099, 25278,
TITLE OF INVENTION: WELL DISORDERS USING 118926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION: 12030, 985, 11237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION: 12030, 985, 11237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION NUMBER: US/11/302,678
CURRENT FILING DATE: 2005-01-14
PRIOR PILING DATE: 2002-01-16
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
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PRIOR PILING DATE: 2002-11-05
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PRIOR PILING DATE: 2002-11-16

                          GlnTrpPheAsnSerPheValAsnProPheLeuTyrProLeuCysHisArgArgPheGln 368
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---CTGGCGACCATCCTCCGTGTACGCACCTTCCACCGCGTGCCCCACAACCTGGTGGCA 303
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                              Sequence 37, Application US/11302678 Publication No. US20060088881A1 GENERAL INFORMATION:
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295.50
44.1%
24.2%
14.4%
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; LOCATION: (64)...(1137)
US-11-302-678-37
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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APPLICANT: Healy, Alleen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hearaclogical Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: Hearaclogical Disorders Using 232, 304, 1980, 14717, 9941, 1931C
FILE REFERENCE: MPIZO10-288PIRCPIOMNIM
CURRENT APPLICATION NUMBER: US/11/242,505A
CURRENT FILING DATE: 2005-10-03
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 10/320,351
PRIOR FILING DATE: 2001-12-16
PRIOR PLING DATE: 2001-12-16
PRIOR PLING DATE: 2001-12-17
SOFTWARE FRANCE FILING DATE: 2001-12-17
SOFTWARE FRANCE FILING DATE: 2001-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        943 CACGTCATCTCCCGGCATCTTCTTCTACCTGGGCGGCCAACCCCGTGCTCTATAGC 1002
182 LeuLeuGluPheLeuLeuPro-----ValIleSerValAlaTyrPheAsnValGlnIle 199
                                                                                                200 TyrTrpSerLeuTrpLysArgArgAlaLeuSerArgCysProSerHisAlaGlyPheSer 219
                                                                                                                                                                                                   220 ThrThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSer 239
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                                                                                                                                                                                                                                                 ------GGGCTGCGACTGCGGCGGGAG 714
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                          1003 CTCATGTCCAGCCGCTTCCGAGAGACCTTCCAGGAGGCCCTGTGCCTC 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Carroll, Joseph M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
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                       TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 CCCCTGGAGCTCTATGAGATGTGGCACACAACTACCCCTTCCTGCTGGCGTTGGTGGCTGC 333
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                     TILLE REPRENCE: MPI2001-288PIRCPLOWNIM
CURRENT APPLICATION NUMBER: US/11/242,505A
CURRENT FILING DATE: 2005-10-03
PRIOR APPLICATION NUMBER: US 10/290,078
PRIOR PELING DATE: 2002-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1212
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236.50
36.3%
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Healy, Aileen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Willennium Pharmaceuticals, Inc.
APPLICANT: Venkateswarlu, Karichei, Biogones Valor, Silos-Santiago, Inmaculada
APPLICANT: Venkateswarlu, Karichei, Biogones Valor, Silos-Santia, Silos-Santia, Discontrol, Biogones Valor, Arabis, 593, 34021, 44099, 25278,
TITLE OF INVENTION: WORGACIGLE DISCONDES, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION: 12030, 985, 11237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION: 12030, 985, 11237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION: 12030, 985, 11237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
TITLE OF INVENTION NUMBER: US 60/349, 511
RRIOR RELIGATION NUMBER: US 60/340, 511
RRIOR PELICATION NUMBER: US 60/360, 603
RRIOR PELICATION NUMBER: US 60/403, 468
RRIOR PELING DATE: 2002-04-19
RRIOR PELING DATE: 2002-08-14
RRIOR PELING DATE: 2002-08-14
RRIOR PELICATION NUMBER: US 60/419, 986
RRIOR PELICATION NUMBER: US 60/419, 986
RRIOR PELICATION NUMBER: US 60/429, 797
RRIOR PELICATION NUMBER: US 60/429, 997
RRIOR PELICATION NUMBER: US 60/429, 797
RRIOR RELIGE DATE: 2002-11-05
RRIOR RELIGE DATE: 2002-11-05
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                                                                                                                                                     802 GGCCGGAGACAAGTGACCAAGATGCTGTTTGTCCTGGTCGTGGTTTTGGCATCTGCTGG 861
                                                                                                                                                                                                                                                              ----CACGCCGACCGC 882
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                             ::: ||||:::||| ::: TACACCTGCAGGCACGACAGCACGAT------CGG
  SerPheTrpArgSerGluSerAlaAlaLeuArgGlnArgGluTyrAlaGluLeuLeuArg
                                                                                                    GlyArgLys---LeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrp
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Matches:
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; Sequence 21, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
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ORGANISM: Homo Sapiens
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US-11-302-678-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 ThrThrSerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSer 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 AsnProGlyLeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSer 259
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214 ACCAACTACTACTCTTCAGCCTGGCCGTGTCTGCTGCTGCTGGTGGGCCTG
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Indels:
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Best Local Similarity:
Query Match:
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; LOCATION: (1)
US-11-242-505A-17
                                                                              Alignment Scores:
Pred. No.:
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COMPOSITIONS FOR TREATING
DISORDERS USING 1435, 559, 34021, 44099, 25278,
55089, 21407, 42032, 46656, 62553, 302, 323,
113237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
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                                                                                                   PheTrpLeulleThrAspTyrLeuLeuCysThrAlaSerValTyrAsnIleValLeulle 108
                                                                                                                                                       SerTyrAspArgTyrGlnSerValSerAsn-----AlaValSerTyrArgAlaGln 125
                                                                                                                                                                                                       HisThrGly11eMetLys1leValAlaGlnMetValAlaValTrp11eLeuAlaPheLeu 145
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SerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPheLeuValGlyLeuIleSerIle
                                                                                                                   ProLeuTyrIleProHisValleuPheAsn---TrpAsnPheGlySerGlyIleCysMet
                                                                                                                                                                    ValAsn---GlyProMetIleLeuAlaSerAspSerTrpLysAsnSerThrAsnThrLys
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US-11-304-129-35 ; Sequence 35, Application US/11304129 ; Publication No. US20060088915A1

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GENERAL INFUGARATION
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APPLICANT: MASUDA, Yasushi
APPLICANT: TAKATSU, Yoshihiro
APPLICANT: TAKATSU, Yoshihiro
APPLICANT: TERAO, Yasushi
APPLICANT: BINTANI, Yasushi
APPLICANT: BINTANI, Yasushi
APPLICANT: BINTANI, Yasushi
ITTLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
FILE REFERENCE: 2762USOP
CURRENT APPLICATION NUMBER: US/11/304,129
CURRENT APPLICATION NUMBER: US/203
FRIOR APPLICATION NUMBER: US/203
FRIOR APPLICATION NUMBER: US 2000-217442
FRIOR APPLICATION NUMBER: UP 2000-21742
FRIOR APPLICATION NUMBER: UP 2001-26779
FRIOR APPLICATION NUMBER: UP 2001-0675
FRIOR APPLICATION NUMBER: UP 2001-06779
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FRIOR FILING DATE: 2001-07-18
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Slos-Santiago, Inmaculada
APPLICANT: Slos-Santiago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION: 12245, 1379, 41897, 47174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION: 3424 MOLECULES
TITLE OF INVENTION: 13424 MOLECULES
TITLE OF INVENTION: 13424 MOLECULES
CURRENT APPLICATION NUMBER: US/11/312,958
CURRENT FILING DATE: 2005-12-29
PRIOR FILING DATE: 2003-02-19
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LeuGluPheLeuLeuProVallleSerValAlaTyrPheAsnValGlnIleTyrTrpSer 202
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                  PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR PELING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373,010
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ELLING DATE: 2002-04-16
APPLICATION NUMBER: US 60/373,908
APPLICATION NUMBER: US 60/377,717
FILING DATE: 2002-05-03
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PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR PILING DATE: 2002-05-21
PRIOR FILING DATE: 2002-06-03
PRIOR FILING DATE: 2002-06-03
PRIOR PILING DATE: 2002-06-06
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619 GCAGTGGTCATCCACTTCCTCCTCCTCCTGTCGTGTCCTTCTGCTACCTGCGC 678
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                              See File Wrapper
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Mismatches:
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PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 64
SUFTARRE: FastSEQ for Windows Version 4.0
LENGTH: 1105
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US-11-312-958-23
                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2002-02-03-33

PRIOR FILING DATE: 2002-02-03-33

PRIOR FILING DATE: 2002-04-04

PRIOR FILING DATE: 2002-04-16

PRIOR PAPLICATION NUMBER: US 60/373,908

PRIOR FILING DATE: 2002-04-18

PRIOR PAPLICATION NUMBER: US 60/373,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             976 ACCTCACTGCCTTCTACGTGGTCGAGTGCATCGCCATGACAGCATGATCAACACG 1035
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                                                                                  -----TGTGCTATGCCAGGA 780
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                                                                                                                                 243 LeuLysGluSerAlaAlaSerArgHisSerGluSerProArgArgLysSerSerIleLeu 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 ysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrC 322
                                 SerSerAlaSerGlyHisLeuHisArgAlaGlyValAlaCysArgThrSerAsnProGly
                                                                                                                                                                                                                                          ValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysValGlySerPheTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 ysLeuPheThrIleValLeuSerThrTyrProArgThrGluArgProLysSerValTrpT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919 ACGGTTTCACCATCGTTCGTGACTTCTCCCC---ACTGTGTTCGTGAAGGAAAAGCACT
                                                                                                                                                                                      1096 ACTGGCGTCCC----TCCCAGCGGGGGGCAGTCCAGT 1130
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APPLICATION NUMBER: US 60/379,949
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APPLICATION NUMBER: US 60/385,280
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APPLICATION NUMBER: US 60/386,879
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US-11-312-958-11       Alignment Scores:       2.23e-10       Length:       1727         Pred. No.:       206.00       Marches:       77         Percent Similarity:       36.9\$       Conservative:       66         Best Local Similarity:       19.8\$       Mismatches:       147         Query Match:       10.1\$       Indels:       98         DB:       7       Gaps:       13	10-626-445-8 (1-391) x US-11-312-958-11 (1-1727)  19 AlaPheLeuMetSerSerPheAlaPheAlaIleMetValGlyAsnAlaVal	0	
Db 712 GCCAAGCCA 720  Qy 259 SerSerIleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysVal 278  Qy 259 SerSerIleLeuValSerLeuArgThrHisMetAsnSerSerIleThrAlaPheLysVal 278	299 ArgGlyArgLysLeuAlaArgSerLeuAlaIleLeuLeuSerAlaPheAlaIleCysTrp 775	PSES CCCATTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT	

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871 ATCAAGATGTTGATGCTGGTGGTAGTCCTTTTGCCCTCTGCTGGTTCCCCCTCAACTGC 930
                   364 HisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysTrpProAlaLeu 383
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